5.1.6 Compugen Ltd.		December 23, 2005, 23:11:27; Search time 230 Seconds (without alignments) 1165.655 Million cell updates/sec
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	using sw model	2005, 23:11:27 ()
Copyright (OM protein - protein search, using sw model	December 23,
	OM protein	Run on:

1 MTFRSLLQEMRSRPHRVVHA......SAFQAFAICLSSFETRIACE 380 US-10-763-042-9 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

79

SUMMARIES

1				~	Q8h485 oryza sativ	oryza					oryza	Q9st78 oryza sativ					m								-	~	_	arabid	oryza	7 oryza
Q9SQU1 ARATH	Q6NPQ1_ARATH		Q8VY21_ARATH	O82257_ARATH				Q9ZP59	Q9FRH7	QBLJA9					Q7Y213_	094483	Q9SXI3	ОЭМЗНЭ	Q84JM8	Q9C6B4	Q84JT0	Q84UG3_	Q84UG2	Q622G9	Q9ZPW1	Q93VI8			Q68Y48	
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Q8YZ21_ARATH Q6NYZ1 Q8Z257 ARATH Q6NYZ1 1015 51.7 445 2 Q8Z46_ORYSA Q6N485 Q8Z257 ARATH Q6NYZ1 1013.5 51.7 445 2 Q8Z46_ORYSA Q6NZ46 Q99.5 50.9 445 2 Q9ZFH7_ARATH Q6NZ46 Q9154 Q99.5 50.6 448 2 Q9ZFH7_ARATH Q9NZ46 Q9Z59 Q9Z 50.6 448 2 Q9ZFH7_ARATH Q9Z559 Q7Z51Z ARATH Q6NZ67 Q9Z76 Q9Z776 Q9Z76 Q9Z776 Q9Z77</td><td>1 1962 100.0 380 2 QSSQUIJ ARATH QGBQUIJ 3 1442.5 73.5 389 2 QGNVX7 ARATH QGNYX7 4 1149.5 72.1 380 2 QGNXX7 ARATH QGNYX7 5 1139 58.6 407 2 QBYX21 ARATH QGBYXX7 6 1139 58.1 406 2 QBH485 QRXSA QBA557 1 1013.5 51.7 445 2 QSPKSA QGB054 QBA565 1 1013.5 51.7 445 2 QT5HX5 QRXSA QFFHA9 QFFHA9 1 1013.5 51.7 445 2 QT5HX5 QRXSA QFFHA9 QFFHA9 QFFHA9 1 999.5 50.6 448 2 QTXSVA QRXSA QFFHA9 QFFHA9 1 989 50.4 462 2 QTXSVA QRXSA QRXSA QS</td><td>1 1962 100.0 380 2 Q6NPQI_ARATH Q6mpqI 3 144.5 72.1 389 2 Q6NNX7 ARATH Q6mpqI 4 144.5 72.1 380 2 Q6NNX7 ARATH Q6mpqI 5 1147.5 58.5 407 2 Q6NX7 ARATH Q6mpqI 6 1139 58.1 406 2 Q8H485 Q8Mp48 Q8D48 7 1015 51.7 455 2 Q6Mp48 Q6mp48 10 999.5 50.9 448 2 Q75MX5 Q69u54 10 999.5 50.9 448 2 Q75MX5 Q6mb48 Q6mb48 10 999.5 50.4 462 2 Q9TRHT Q9TRHT Q9TRHT 10 999.5 50.4 462 2 Q9TRHT Q9TRT Q9TRT 11 969.5 49.4 440 2 Q8TMSA Q6TRT</td></th<>	1 1962 100.0 380 2 QSSQUI ARATH QGFQUI 3 1442.5 73.5 389 2 QGFWX7 ARATH QGFWX7 4 144.5 72.1 380 2 QGFWX7 ARATH QGFWX7 5 114.5 58.5 407 2 QBFWX7 ARATH QGFWX7 6 1139 58.1 406 2 QBHABS QRFWXA QBBAS 7 1015 58.1 466 2 QBFWA QBBAS QBBAS 10 999.5 50.9 445 2 QFRMA QFSDS QBSSDS 11 999.5 50.4 462 2 QPSTMA QBSDS QBSDS 12 989 50.4 462 2 QPSTMA QBSTMA QBSTMA 13 989 50.4 462 2 QSTMS QBSTMA QBSTMA 14 960 50.4 462 2 Q	1 1962 100.0 380 2 Q9SQUI ARATH Q6npq1 3 144.5 73.5 389 2 Q6NWZ7 ARATH Q6npq1 3 144.5 72.1 380 2 Q6NWZ7 ARATH Q6npq1 5 8.6 406 2 Q8VY21_ARATH Q6npq1 6 1139 58.6 407 2 Q8YZ1_ARATH Q6NYZ1 ARATH Q6NYZ1 1139 58.1 406 2 Q8YZ21_ARATH Q6NYZ1 Q8Z257 ARATH Q6NYZ1 1015 51.7 445 2 Q8Z46_ORYSA Q6N485 Q8Z257 ARATH Q6NYZ1 1013.5 51.7 445 2 Q8Z46_ORYSA Q6NZ46 Q99.5 50.9 445 2 Q9ZFH7_ARATH Q6NZ46 Q9154 Q99.5 50.6 448 2 Q9ZFH7_ARATH Q9NZ46 Q9Z59 Q9Z 50.6 448 2 Q9ZFH7_ARATH Q9Z559 Q7Z51Z ARATH Q6NZ67 Q9Z76 Q9Z776 Q9Z76 Q9Z776 Q9Z77	1 1962 100.0 380 2 QSSQUIJ ARATH QGBQUIJ 3 1442.5 73.5 389 2 QGNVX7 ARATH QGNYX7 4 1149.5 72.1 380 2 QGNXX7 ARATH QGNYX7 5 1139 58.6 407 2 QBYX21 ARATH QGBYXX7 6 1139 58.1 406 2 QBH485 QRXSA QBA557 1 1013.5 51.7 445 2 QSPKSA QGB054 QBA565 1 1013.5 51.7 445 2 QT5HX5 QRXSA QFFHA9 QFFHA9 1 1013.5 51.7 445 2 QT5HX5 QRXSA QFFHA9 QFFHA9 QFFHA9 1 999.5 50.6 448 2 QTXSVA QRXSA QFFHA9 QFFHA9 1 989 50.4 462 2 QTXSVA QRXSA QRXSA QS	1 1962 100.0 380 2 Q6NPQI_ARATH Q6mpqI 3 144.5 72.1 389 2 Q6NNX7 ARATH Q6mpqI 4 144.5 72.1 380 2 Q6NNX7 ARATH Q6mpqI 5 1147.5 58.5 407 2 Q6NX7 ARATH Q6mpqI 6 1139 58.1 406 2 Q8H485 Q8Mp48 Q8D48 7 1015 51.7 455 2 Q6Mp48 Q6mp48 10 999.5 50.9 448 2 Q75MX5 Q69u54 10 999.5 50.9 448 2 Q75MX5 Q6mb48 Q6mb48 10 999.5 50.4 462 2 Q9TRHT Q9TRHT Q9TRHT 10 999.5 50.4 462 2 Q9TRHT Q9TRT Q9TRT 11 969.5 49.4 440 2 Q8TMSA Q6TRT

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121 YLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTV 180

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	ALIGNMENTS					
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Q9h4d2 homo sapien	Q9H4D2 HUMAN	7	420	22.3	437.5	45
Q6dee2 xenopus lae	Q6DBE2_XENLA	7	206	22.5	440.5	44
P46686 mus musculu	TULP2 MOUSE	-	564	22.5	441.5	43
Q8c5r9 mus musculu	Q8C5R9_MOUSE	~	562	22.5	441.5	42
Q8c5r7 mus musculu	Q8C5R7_MOUSE	7	269	22.5	441.5	41
Q484q7 tetraodon n	Q4S4Q7_TETNG	~	540	22.9	450	40
_	QSFW93 MOUSE	N	438	23.2	455.5	33
	OSXFX6_RAT	N	486	23.2	456	38
	Q6Z2H0_ORYSA	~	326	28.8	565.5	37
Q8w220 pyrus commu	Q8W220_PYRCO	~	219	30.4	596.5	36
Q8h0w5 arabidopsis	Q8H0W5_ARATH	N	267	32.5	637.5	35
Q94dt9 oryza sativ	Q94DT9 ORYSA	N	368	36.9	723	34
~	Q53PP4 ORYSA	N	317	36.9	723.5	33
CAVITA GIGOTOPIA	QSALFS AKATH	4	415	40.1	787.5	32

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61 NVVACAGVCRSWRILLTKEIVAVPEPSSKLIFPISLKQSGPRDSLVQCFIKRNRNTQSYHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTFRSILQEMRSRPHRVVHAAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSRR
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                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-FEB-2000 (TrEMBLrel. 29, Last annotation update)
F24P17.15 protein (Tubpy-like protein TULP9).
Name=F24P17.15, Synonyms=TULP9;
Name=F24P17.15, Synonyms=TULP9;
Evabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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М.Е.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15064372; DOI=10.1104/pp.103.037820;
Lai C.P., Lee C.L., Chen P.H., Wu S.H., Yang C.C., Shaw J.F.;
"Molecular analyses of the Arabidopsis TUBBY-like protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1962; DB 2; Length 380; Best Local Similarity 100.0%; Pred. No. 5.3e-165; Matches 380; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                       Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas Roming C.M., Koo H., Pujii C.Y., Uterback T.R., Barnstead Bowman C.L., White O., Nierman W.C., Fraser C.M.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JB 1; UNKNOWN 1.
42310 MW; EDB57859F8B5F51D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC011623; AAF08576.1; -; Genomic_DNA.
EMBL; AC011623; AAF08576.1; -; Genomic_DNA.
EMBL; AR487270; AAQ66243.1; -; mRNA.
HSSP; P505865; 1178.
GO; GO:0045449; P:regulation of transcription; TAS.
InterPro; IPR001810; P-box.
InterPro; IPR0000007; Tubby.
Pfam; PF00167; Tubby.
Pfam; PF00167; Tub; 1.
PRINTS; PR01573; SUPERTUBRY.
PROSITE; P8012073; TUB; 1.
PROSITE; P8012073; TUB; 1.
PROSITE; B801200; TUB; 1. UNKNOWN 1.
SEQUENCE 380 AA; 42310 MM; EDBS7859F8B5F51D CRC64;
                                     380 AA.
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              11 ARATH
Q9SQU1_ARATH PRELIMINARY;
Q9SQU1;
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NUCLEOTIDE SEQUENCE.
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RESULT 1
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61 ACAGVCRGWRLLMNETVVVVPELSSKITFPISLKQPGPRDSLVQCFIKRNRITQSYHLYLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S---QTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIPM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEQLRCWCLNFHGRVTVASVKNFQLVAV-SDCEAG-----QTSERIILQFGKVGKDMFT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLYLG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 LITSLIDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDG 183
241 QCLMDTIPTSTMEPQGVASEPSEFPLLGTRSTLSRSQSKPLRSSS-----SHLKETPL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLSNKAPRWHEQLRCMCLNFHGRVTVASVKNFQLVAV-SDCEAG-----QTSERIILQF
                                                                    10 MRSRPHRVVH-----AAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSRRNVV
                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tubby-like protein 12.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Subaryota, Virialplantae; Streptophyra, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15064372; DOI=10.1104/pp.103.037820;
Lai C.P., Lee C.L., Chen P.H., Wu S.H., Yang C.C., Shaw J.F.;
"Molecular analyses of the Arabidopsis TUBBY-like protein gene
family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.1%; Score 1414.5; DB 2; Length 72.9%; Pred. No. 1.7e-116; ive 31; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUB 1; UNKNOWN 1.
; 41993 MW; EFS2AA224CDA8F4D CRC64;
                                                                                                                                         MDYGYPISAFQAFAICLSSFETRIACE 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AY046922, AAL03978.1; -; mRNA.
GO; GO:0006512; P:ubhquitin cycle; IEA.
InterPro; IPR001810; F-box.
InterPro; IPR000007; Tubby.
                                                                                                                                                                                                                                                                                                                                                         Created)
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QGYNX7;
05-JUL-2004 (TrEMBLrell. 27,
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PROSITE; PS01200; TUB 1; UNK
SEQUENCE 380 AA; 41993 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 72.99
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Pfam; PF01167; Tub; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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Matches
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Q6YNX7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIPM 240
                                                                                                                     300
                                                                                                                                                                                                                  HEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEAGQTSERIILQFGKVGKDMFTMDYGYPI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 DWPSRRNVVACAGVCRSWRILIKEIVAVPEFSSKLIFPISLKQSGPRDSLVQCFIKRNRN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GTKFTVFDGS---QTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRM 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCIMDIIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPL 291
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                                                                                                                                                                                                                                           301 HEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEAGQTSERIILQFGKVGKDMFTMDXGYPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTFRSLLQEMRSRPHRVVH-----AAASTANSSDPFSWSELPEELLREILIRVETVDGG
                          FDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIPM
                                                                                                                        SIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRW
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.

Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;

"Arabidopsis ORF clones";

Submitted (FBE-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BT010768; AAR23738.1; -; mRNA.

EMBL; BT020601; AAW80874.1; -; mRNA.

EMBL; Prubiquitin cycle; IEA.

InterPro; IPR001810; F-box.
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Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF00646; Pbox; 1.
Pfam; PF0167; Tub; 1.
PRINTS; PR01573; SUPERTUBBY.
PROSITE; PS01200; TUB 1; UNKNOWN 1.
PROSITE; PS01200; TUB 1; UNKNOWN 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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                                                                                                                                                                                                                                                                                                               361 SAFQAFAICLSSFETRIACE 380
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QENPOL;
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Gaps

63 9

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120 GSLVQCYIMRNRSNQTYYLYLGLNQAAASNDDGKFLLAAKRFRRPTCTDYIISLNCDDVS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GSNTYIGKLRSNFLGTKFTVYDAQPTNPGTQVTRTRSSRLLSLKQVSPRIPSGNYPVAHI
                                                                SYELINVLGSRGPRRMRCIMDTIPMSIVESRGV-----VASTSISSFSSRSSPVFRSHSK
                                                                                               240 SYELNVLGSRGPRRNQCVMDAIPASAVEPGGTAPTQTELVHSNLDSFPSFS--FFR--SK
                                                                                                                                                                                       271 PLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAV-S
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Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Cready T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Roumsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M., Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C., Submitted (MAR-2000) to the EMBL/GenBank/DDEJ databases.
                                                                                                                                                                                                                                                                                                                     380
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                                                                                                                                                                                                                                                                                                                                                       356 NGPAGPEHENVILQFGKVGKOVFTWDYQYPISAFQAFTICLSSFDTKIACE
                                                                                                                                                                                                                                                                                                                         330 DCEAGQISERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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EMBL; AC006072; AAM15124.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407
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GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro: IPR001810; P-box.
InterPro; IPR000007; Tubby.
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Arabidopsis thaliana (Mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   082257 ARATH PRELIMINARY;
082257;
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Pfam; PF01167; Tub; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSLVQCFIKRNRNTQSYHLYLGLTTSLT-DNGKFLLAASKLKRATCTDYIISLRSDDISK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSNAYLGRMRSNFLGTKFTVFDGSQTG-AAKMQKSRSSNFI---KVSPRVPQGSYPIAHI 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTFRSLLQEM-------RSRPHRVVHAAASTANSSDPFSWSELPBELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nameda K., Banh J., Chan M.M., Chang C.H., Chang B., Dale J.M., Deng J.M., Banh J., Chan M.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yammaura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Meyers M.C., Miranda M., Narusaka M., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Submitted (Apr. 2002) to the RNBL/GenBank/DDBJ databases.

EMBL, AY04273; AAL669701; -; mRNA.

EMBL, AY04274; AAK98802.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tubby-like protein 3.

Name=At2g47900;

Name=At2g47900;

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15064372; DOI=10.1104/pp.103.037820;
Lai C.P., Lee C.L., Chen P.H., Wu S.H., Yang C.C., Shaw J.F.;
"Molecular analyses of the Arabidopsis TUBBY-like protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 AA; 45311 MW; C8A8188C0A0D77D4 CRC64;
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                                                                                                                                                                                           Last sequence update)
Last annotation update)
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GO; GO:0045449; P:regulation of transcription; TAS.
InterPro; IPR001810; F-box.
InterPro; IPR000007; Tubby.
Pfam; PF00646; F-box; 1.
Pfam; PF01167; Tub; 1.
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                                                                                               406
                                                                                               PRT;
                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Physiol. 134:1586-1597(2004)
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                                                                                        QBVY21 ARATH PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE. Yamada K., Liu S.X.,
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326 ANQGEDDIPEAKERPLVLRNKVPRWHEQLQCWCLNFRGRVTVASVKNFQLIAAASSESS 385
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                              271 PLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSD 330
                                                                  92 AVCRIWREICKDIVQSPEICGKLIFPVSLKQPGPRDGLIQCFIKRDKSKLTYYLYLCLGP 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 LSELEDRPVVV------DQSRWVGLPPELLRDVMKRLEEGE-SNWPSRKDVVACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 GNNLGDP-----PLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LOEMRSRPHRVVHAAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSRRNVVACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Boprmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative chain A, C-terminal domain of mouse brain tubby protein.
Name=P0015C07.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                         331 CE-AGQISERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE
                                                                                                                                                                                           / Match 51.7%; Score 1015; DB 2; Length 451; Local Similarity 49.8%; Pred. No. 5.2e-81; les 212; Conservative 57; Mismatches 87; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone:P0015C07.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004654; BAD33172.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1573; SUPERTUBBY.
PROSITE; PS01200; TUB 1; UNKNOWN 1.
PROSITE; PS01201; TUB 2; 1.
PROSITE; PS01201; TUB 2; 1.
SEQUENCE 451 AA, 50528 MW, F875D1FB652E881E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare (GA3) genomic DNA, chromosome
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GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR001810; F-box.
InterPro; IPR0000007; Tubby.
Pfam; PF00646; F-box; 1.
Pfam; PF01167; Tub; 1.
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25-OCT-2004 (TrEMBLrel. 28, Last seq
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                   Q69US4_ORYSA PRELIMINARY;
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                                 180 RGSNTYIGKURSNFLGTKFTVYDAQPTNPGTQVTRTRSSRLLSLKQVSPRIPSGNYPVAH 239
                                                                                                                               ISYELNVLGSRGPRRMRCIMDTIPMSIVESRGV-----VASTSISSFSSRSSPVFRSHS 269
                                                                                                                                                             240 ISYELMVLGSRGPRRMQCVWDAIPASAVEPGGTAPTQTELVHSNLDSFPSFS--FPR--S 295
                                                                                                                                                                                                                                                          270 KPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAV- 328
                                                                                                                                                                                                                                                                                            296 KSIRAESLPSGPSSAAQKEGLLVLKNKAPRWHEQLQCWCLNFNGRVTVASVKNFQLVAAP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ELLREVLARVESSEGW-WPRRRDVVACAGVCRSWRGIVREIVRTPEASGNLTFPISLKQP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 GPRDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKRSNAYLGRMRSNFLGTKFTVFDGSQTGA----AKMOKSRSSNFIKVSPRVPQGSYPIA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 SKRTDSYVGKIRSNFLGTKFTIYDAHPPYAGDVISKGQSARVIGSNHLSPRIPAGNYPVS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 HISYELNVIGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSS----PVFRSHSK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRSNAYLGRMRSNFLGTKFTVFDGSQTG-AAKMQKSRSSNF1---KVSPRVPQGSYPIAH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative tubby related protein.
Name=P0450A04.125;
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                         329 SDCEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE 380
                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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; Pred. No. 4.7e-92;
57; Mismatches 86;
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Submitted (OCT-2001) to the EMBL/GenBank/DI
EMBL; AP004274; BAC20077.1; -; Genomic_DNA
HSSP; P50586; 117E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Sasaki T., Matsumoto T., Yamamoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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PROSITE; PS01200; TUB 1; UNKNOWN 1.
PROSITE; PS01201; TUB 2; UNKNOWN 1.
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Matches 232; Conservative
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Pfam; PF01167; Tub; 1.
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GNNLG---DPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAV-SDCEAGQTS- 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U1-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
F22K20.1 protein (Tub family protein, putative) (At1g76900/F7012_7)
Name=F22K20.1; Synonyms=F7012.7, TULP1;
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              SQPAPPEQDKIILQFGKVAKDMFTMDYRYPLSAFQAFAICLSSFDTKLACE 445
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Lai C.P., Lee C.L., Chen P.H., Wu S.H., Yang C.C., Shaw J.F.;
"Molecular analyses of the Arabidopsis TUBBY-like protein gene
                                                                                                                                                                                                                                              338 -----ERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bcker J.R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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EMBL; AC002291; AAC00626.1; -; Genomic_DNA.

EMBL; AC079283; AAG51146.1; -; Genomic_DNA.
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Q9ZP59;
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Name-OSJNBD0042217.6; Synonyms-OJ1058 F05.11;
Name-OSJNBD0042217.6; Synonyms-OJ1058 F05.11;
Edge transport of the property of the prop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H., Hsing J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu Ji Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F., F., Lin Y.-C., Wu B.-W., Physia Sativa BAC OJ1058 F05 genomic sequence."; Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AC134930; AANO911.1; -; Genomic_DNA.

EMBL, AC105318; AAV59313.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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51.3%; Pred. No. 7e-81;
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GO; GO: 0006512, P: ubiquitin cycle; IRA.
GO: GO: PR001810; P-box.
InterPro; IPR000007; Tubby.
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Pfam; PF01167; Tub; 1.
PRINTS; PR01573; SUPERTUBBY.
PROSITE; PS01200; TUB 1; UNKNOWN 1.
PROSITE; PS01201; TUB 2; 1.
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Molecular analyses of the Arabidopsis TUBBY-like protein gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEELLREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLK
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MSFRSIVRDVRDSIGSLSRRSFDFKLSSLNKEGGKSRGSVQDSHEEQLVVTIQETPWANL
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                                                                                                                                                                                                                                                                                                                       177;
                                                                                                                                                                                                                                                                            DB 2; Length 455;
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Lai C.P., Lee C.L., Chen P.H., Wu S.H., Yang C.C., Shaw J.P.;
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                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-FRB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein F4F7.33 (Tubby-like protein TULP10)
Name=F4F7.33; Synonyms=TULP10;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                              PRINTS; PRO1573; SUPERTUBBY.
PROSITE; PS01200; TUB 1; UNKNOWN 1.
PROSITE; PS01200; TUB 2; 1.
SEQUENCE 455 AA; 51194 MW; 53072DB655960C3E CRC64;
                                               GO; GO:0045449; P:regulation of transcription; TAS.
InterPro; IPR001810; F-box.
InterPro; IPR000007; Tubby.
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                                                                                                                                                                                                                                                                                                                                                                        MTFRSLLQEMR - - - - SRPHRVVHAAASTANSSDPFS-
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Q9FRH7;
                                                                                                                                                                                                                                                                                                                            Matches 215; Conservative
                                                                                              InterPro; IPR000007; Tubb
Pfam; PF00646; F-box; 1.
Pfam; PF01167; Tub; 1.
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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240 PSGSYNIAQITYELNVLGTRGPRRMHCIMNSIPISSLEPGGSVPNQPEKLVPAPYSLDDS 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 LKQSGPRDSLVQCFIKRNRNTQSYHLYLGLTTS-LTDNGKFLLAASKLKRATCTDYIISL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CWCLNFHGRVTVASVKNPQLVAV-----SDCBAGQTS-----ERIILQFGKVGKDM 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLR
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Indels
                                                                                                                                                                                                                                                                                                                                                                                      445 AA; 50010 MW; C77BEA9ED18B9D21 CRC64;
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Last annotation update)
                                                                                                                                      of transcription; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%; Score 999.5; DB 2
47.2%; Pred. No. 1.2e-79;
tive 71; Mismatches 93
EMBL; AC079374; AAC28805.1; -; Genomic_DNA.
EMBL; AC079374; AAC28805.1; -; Genomic_DNA.
EMBL; APG487271; AAQ06244.1; -; mENA.
EMBL; AF687271; AAQ06244.1; -; mENA.
EMBL; AF687271; AAQ06244.1; -; mENA.
EMBL; AF687271; AAQ06244.1; -; mENA.
HSSP; P50586; 117E.
GO; GO:004549; P:regulation of transcription InterPro; IPR001810; P-box.
InterPro; IPR001810; P-box.
InterPro; IPR000007; Tubby.
PFam; PF01167; Tub; 1.
PFINTS. PF01167; Tub; 1.
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                                                                                                                                                                                                                                                                       PRINTS; PRO1573; SUPERTUBBY.
PROSITE; PS01200; TUB_1; UNKNOWN_1
PROSITE; PS01201; TUB_2; 1.
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Q8LJA9_ORYSA PRELIMINARY;
Q8LJA9;
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Matches 212; Conservative
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Query Match
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Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idohuma A., Iijima M., Ikeda M.,
Ikeno M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Rarasawa W., Katagiri S., Kikuta A., Kobayashi N., Komo I.,
Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,
Wari K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Ano M., Jiang J., Gojobori T.;
The genome sequence and structure of rice chromosome 1.";
Nature 420:312-316(2002).
REMBL; APO03270; BAC01219.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 GSYPIAHISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVV------AST
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                                                                                                                                                                                                                                                                                                                                    Length 448;
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448 AA; 49924 MW; 2172769A9CB85892 CRC64;
                                                                                                                                                                                                                                                                                                                                   50.6%; Score 992; DB 2;
48.8%; Pred. No. 5.7e-79;
tive 62; Mismatches 98;
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GO; GO: 0006512; P: ubiquitin cycle; IEA.
InterPro; IPR0010810; P-box.
InterPro; IPR0010917; Tubby.
Pfam; PF00167; Tubby.
Pfam; PF01167; Tub; 1.
                                                                                                                                                                                                                                                                     PRINTS; PRO1573; SUPERTUBBY.
PROSITE; PS01200; TUB 1; UNKNOWN 1.
PROSITE; PS01201; TUB 2; 1.
SEQUENCE 448 AA; 49924 MW; 2172'
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Q7XSV4
01-OCT-2003 (TrEMBLrel. 25, U.S.
01-OCT-2003 (TrEMBLrel. 25, L.S.
01-MRA-2004 (TrEMBLrel. 26, L.S.
OSJNBA0039K24.2 protein.
Name=OSJNBA0039K24.2;
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 48.8°
Matches 219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 EQLRCWCLNFHGRVTVASVKNFQLVAVS------DCEAGQTSER-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 EELLREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 DISKRSNAYLGRMRSNFLGTKFTVFD----GSQTGAAKMQKSRSSNFIKVSPRVPQGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 PIAHISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVV------ASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 ISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLG------DPPLVLSNKAPRWH
                                                                                                                                                           PubMed=12447439; DOI=10.1038/nature01183; Peng Q., Zhang Y., Li Y., Zhu J., Peng Q., Zhang Y., Hao P., Wang S., Thu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Lu X., Zhu B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., GW W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Xang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W., Zhu G., Tu Y., Jia J., Zhu F., Chen W., Lian L., Lai Y., Chen Z., Gu M., Jiang J., Li J., Hong G., Xue Y., Han B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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44.8%; Pred. No. 1.1e-78;
iive 70; Mismatches 93; Indels
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PROSITE; PS01200; TUB_1; UNKNOWN_1.
PROSITE; PS01201; TUB_2; 1.
SEQUENCE 462 AA; 51529 WW; 5B7C863114B8952E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence and analysis of rice chromosome 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 420:316-320(2002).
EMBL; AL606637; CAE01783.1; -; Genomic_DNA.
HSSP; P50586; 117E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene, Q7XSV4; -.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR001810; P-box.
InterPro; IPR000007; Tubby.
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nes 210; Conservative
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Q9ST78 ORYSA
ID Q9ST78_ORYSA PRELIMINARY;
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Pfam; PF00646; F-box; 1.
Pfam; PF01167; Tub; 1.
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Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H., Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Tsitrin T., Bera J., Kim M., Jin S., Fadrosh D., Vuong H., Overton II L., Reardon M., Weaver B., Johri S., Lewis M., Utterback T., Van Aken S. Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Iobst S., de Vazeilles A., White O., Salzberg S., Fraser C.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Tub family, putative.
ORFNames=LOC_Osl1g06420;
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Subaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 DISKRSNAYLGRMRSNFLGTKFTVFD----GSQTGAAKMQKSRSSNFIKVSPRVPQGSY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIAHISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVV---------ASTS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 PIVQVNYELNVLGTRGPRRMQCAMHSIPASAVEPGGIVPGQPKELLPRLFEESFRSMATS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 ISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLG-------DPPLVLSNKAPRWH 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 EQLRCWCLNFHGRVTVASVKNFQLVAVS------DCEAGQTSER----- 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SRPHRVVHAAASTANSSDPF----SWSELP
                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 989; DB 2; Length 462;
; Pred. No. 1.1e-78;
70; Mismatches 93; Indels
                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                                            51513 MW; 456367D114AE59F4 CRC64;
                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ
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GO; GO:0006512; P:ubiquitin cycle; IBA.
InterPro; IPR001810; F-box.
InterPro; IPR000001; Tubby.
Pfam; PF00646; P-box; 1.
Pfam; PF01167; Tub; 1.
                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1573; SUPERTUBBY.
PROSITE; PS01200; TUB 1; UNKNOWN_1.
PROSITE; PS01201; TUB 2; 1.
PROSITE; PS01201; TUB 2; 1.
                                                                                                                                                                                                                Hong G., Chen Z.;
Submitted (Auge1199) to the EME
EMBL; AJ245900; CAB53492.1; -;
HSSP; PS0S86; 117E.
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Q53PP5 (053PP5)
13-SEP-2005 (TEMBLFEL 31
13-SEP-2005 (TEMBLFEL 31
13-SEP-2005 (TEMBLFEL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 44.89
Matches 210; Conservative
                                                                            CAA303719.1 protein.
Name=q3037.19;
                                                                                                         Oryza sativa (Rice).
                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                     STRAIN=DNA;
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                                                                                                                                                                                                                                                       41 LREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGP
                                                                                                                                                                            1 MIFRSILQEM--------RSRPHRWHAAASTANSSDPFSWSELPEEL
                                                                                                                                     Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tubby-like protein 2.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids il; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                   16;
                                                                                               Length 440;
                                                                                               49.4%; Score 969; DB 2; Length 44
46.2%; Pred. No. 6e-77;
ive 72; Mismatches 93; Indels
Buell R.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AC120533; AAX95106.1; -; Genomic_DNA.
SEGUENCE 440 AA; 48955 MW; 9D9D7312F67AB9B4 CRC64;
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                                                                                                                   al Similarity 46.2
207; Conservative
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Created) Last sequence update) Last annotation update)

(TrEMBLrel. 31, (TrEMBLrel. 31, (TrEMBLrel. 31,

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46 IRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPBFSSKLTFPISLKQSGPRDSLV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 QCFIKRNRATATYILYYGLMPSETENDKILLAARRIRRATCTDFIISLSAKNFSRSSSTY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFR--SHSKPLRSNSASCSDS 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 GNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNPQLVAVSDCEAG---QTSER 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 ---IRDQPLVLKNKSPRWHEQLQCWCLNFKGRVTVASVKNFQLVAEIDASLDAPPEEHER 352
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1 MSLKSILRDLKEVRDGLGGISKRSWSKSSHIAPDQTTPPLDNIPQSPWASLPPELLHDII 60
                                                                                                                                                                                                                                                                                                                                                                      1 MTFRSLLQEMR-----SRPHRVVHAAASTANSSDPFS-WSELPEELLREIL 45
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[1]
NUCLEOTIDE SEQUENCE.
PubMed=1564372; DOI=10.1104/pp.103.037820;
Lai C.P., Lee C.L., Chen P.H., Wu S.H., Yang C.C., Shaw J.F.;
"Molecular analyses of the Arabidopsis TUBBY-like protein gene
                                                                                                                                                                                                                                                                                                      / Match 49.3%; Score 966.5; DB 2; Length 394; Local Similarity 50.1%; Pred. No. 8.5e-77; les 201; Conservative 64; Mismatches 107; Indels 29.
                                                                          family.";
Plant Physiol. 134:1586-1597(2004).
EMBL; AVG45773; AAK98801.1; -; mRNA.
HSSP; P50586; 1178.
GO; GO:0045449; P:regulation of transcription; TAS.
InterPro; IPR001810; F-box.
InterPro; IPR001810; F-box.
InterPro; IPR006007; Tubby.
R Pfam; PF0167; Tubby.
R PRINTS; PR01573; SUPERTUBBY.
R PRNTS; PR01573; SUPERTUBBY.
R PROSITE; P501201; TUB_2; UNKNOWN 1.
R PROSITE; P501201; TUB_2; UNKNOWN 1.
R PROSITE; P501201; TUB_2; UNKNOWN 1.
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Search completed: December 23, 2005, 23:27:49 Job time: 235 secs

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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 506 amino acids
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STRANDEDNESS: single
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MOLECULE TYPE: protein
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Best Local Similarity
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Sequence 7, Appli
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                                                                                                                                                                                                                                                                           1 MTFRSLLQEMRSRPHRVVHA......SAFQAFAICLSSFETRIACE 380
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Compugen Ltd.
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US-08-712-991-7
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GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                      Copyright
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                                                                                                                                                                                                                            Title:
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30	436.5	22.2	505		US-08-936-706A-2	Sequence 2, Appl
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32	4.46.5	7.7			US-U9-U3Z-355A-4	4, (
2 6	426.5	200	מ מ		TC-00-406-021-3	
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, e	423	21.6	460		118-09-270-767-45069	450
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4 6	418	21.0	285		115-08-829-553-15	Semience 15. Apr
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					ALIGNMENTS	
RESULT 1						
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; Sequen	Sequence 19, Application US/09032365A	Applicat	ion US,	00	032365A	
; Patent	No. 61	14502				
CENER .	GENERAL INFORMATION:	EMATTON:			•	
; APE	APPLICANT:	o Z	6114502th,		Michael	
; APE	PLICANT:		la, Patsy	<u>ج</u>		
; APE	APPLICANT:	Naggart,	t, Juergen	<u>5</u>		
; APF	APPLICANT:	CANT: No. 6114	ഗ		Konrad	
ril ;	TITLE OF I	NVENTION		M M	GENE FAMILY ASSOCIATED WITH	
; TIT	TITLE OF II	NVENTION		SSS	NEUROSENSORY DEFECTS	
NON .	NUMBER OF	OF SEQUENCES: 6	S: 67			
. CON	CORRESPONDENCE	ENCE ADD		1		
•	ADDRESSEE:	B: Bozi		e e	LLP	
.,		285 Hamilton	ilton	Ave	Avenue, Suite 200	
٠.	CITY: Pa	Palo Alto	_			
<i>.</i> ,		ä				
٠.	COUNTRY:	USA				
	ZIP: 94	94301				
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Σ.	MEDIUM TYPE:	YPE: Di	Diskette			
٠.	COMPUTER:	: IBM C	IBM Compatible	ole		
	OPERATING SYSTEM:	SYSTEM	500			
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	APPLICATION NUMBER :	AMETER NOT	ER. III	0/5	11S/09/032.365A	
	PILING DATE.	TT.		5		
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TTA	ATTORNEY/AGENT INFORMATION:	SENT INF	CEMATT	ż		
	NAME: S	Sherwood Domesta	Dame			
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	REFERENCE / DOCKET NIMBER -	E/DOCKET	NIME		SE0-20192	
100	NOTE AND INTERNATIONAL PARTIES		TNEODWATTON	Ť		
121	TECOMMON.		1NFORMAL	10		
	TELEPHONE:	950	36/-34	3		
	TELEFAX:	650 327	7-3231			
	TELEX:					
; INFOR	INFORMATION FOR SEQ	FOR SEQ	ID NO:	19		
,	E DUMBLICA	ひつかい くりんひ	DUTTOT			

Length 506;

Score 441.5; DB 2; Pred. No. 1.8e-40;

22.5%; 36.9%;

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132 GK--FLIAASKIKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAA 189
247 GKKVFLLAGRKRKKKKKKSKTSNYLISVDPTDLSRGGDSYIGKLRSNLMGTKFTVYD----NGV 302
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                                                                                                                                                  --RED 246
                                                                                                                                                                                                            249 VASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWC 308
                                                                                                                                                                                                                                                      353 ---VSİRPRNEHETLLARWQNK----NTESI------IELQNKTPVWNDDTQSYV 394
                                                                                                                            190 KMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIP-MSIVESRGV
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201 EVQDLEEFALR------PAPQGITIKCRITRDKKGMDRGMYPTYFLHLD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: NORTH, Michael
APPLICANT: NISHINA, Patsy
APPLICANT: NISHINA, Patsy
APPLICANT: NISHINA, Patsy
APPLICANT: NAGGERT, Juergen
TITLE OF INVENTION: OBESITY ASSOCIATED GENES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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34.9%; Pred. No. 4.3e-40;
tive 60; Mismatches 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08714991
Patent No. 5776762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIPTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SHERWOOD, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-57
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415-494-8700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 amino acids
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449 ALSSFDSKLACE 460
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 109; Conservi
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STATE: Ca
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-714-991-7
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                                         100 PRDSLVQCFIKRNRNTQ----SYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISL 153
                                                                                                                                                      318 DPKDMSRNGSNFVGKVRSNVLGTKFTIFDNG-----VNPERSYWVDDSARIRE--EL 367
                                                                                                                                                                                                                                                      ------LPGMDSRKQ---RMKVQPQN 405
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                                                                                                                            154 RSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPI 213
                                                                                                                                                                                                               214 AHISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLR 273
                                                                                                                                                                                                                                                                                                 274 SNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEA 333
                                                                                                                                                                                                                                                                                                                                         406 DQDSILSRVQKGAĞHGLLLLQNKAPSWSDESGAYVLNFHĞRVTRASVKNFQIVHPDE--- 462
                                                                     261 PRDHWVQWRIVRNKHGMDKGMFPSYYLYLEGEDGV---AHFLLLAGRKRKRSKTSNYLISL
    Gaps
  47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.3%; Score 437.5; DB 1; Length 460; 34.9%; Pred. No. 4.3e-40; tive 60; Mismatches 82; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                          ---PDHLVLQFGRVAPNIFTMDFRYPLCPLQAFAICLSSFDGKLACE 506
                                                                                                                                                                                                                                                                                                                                                                                    334 GQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE 380
  90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISBE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT: 3400 Embarcadero Center, Suite 3400
San Prancisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/630,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 EIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REGISTRATION NUMBER: 36,677
REERENCE/DOCKET NUMBER: A59504/BIR/PJS
TELEFAN: (415) 7811989
TELEFAX: (416) 3983249
SIELEX: 910 277299
SIELEX: 910 277299
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nishina, Patsy
APPLICANT: No. 5770432enTrauth, Konrad
APPLICANT: Naggert, Juergen
APPLICANT: No. 5770432th, Michael
APPLICANT: No. 5770432th, Michael
NUMBER OF INVENTION: Obesity Associated Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
  Mismatches
                                                                                                                                                                                                                                         368 GVVCYETNVLGFRGPRKMTVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 941114187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PCDOS/MSDOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08630592
Patent No. 5770432
      44;
    Conservative
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STREET: 340
    106;
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Best Local S:
Matches 109
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FOR THE TREATMENT AND BODY WEIGHT DISORDERS, INCLUDING OBESITY
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                                                                                                                                                                                                                                                                                                                                                                                                     249 VASTSISSPSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                         353 ---VSIRPRNEHETLLARWQNK----NTESI------IELQNKTPVWNDDTQSYV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNFHGRVTVASVKNPQLVAVSDCEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 EIVAVPEFSSKLIFPISLKOSGPRDSLVQCFIKRNRNTQ-----SYHLYLGLITSLIDN 131
                                                                                               190 KMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIP-MSIVESRGV
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82;
     60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF BODY WE
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08631200 Patent No. 5646040
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TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 amino acids
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449 ALSSFDSKLACE 460
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Best Local Similarity 34.9°
Matches 109; Conservative
     109; Conservative
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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     Matches
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                                                        GK--FLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAA 189
                                                                                         247 GKKVFILAGRKRKKSKTSNYLISVDPTDLSRGGDSYIGKLRSNLMGTKFTVYD----NGV 302
                                                                                                                                                                      190 KMOKSRSSNPIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIP-MSIVESRGV 248
                                                                                                                                                                                                       249 VASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWC 308
                                                                                                                                                                                                                                                                                                                           353 ---VSIRPRNEHETLLARWQNK----NTESI------IELQNKTPVWNDDTQSYV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PAPQGITIKCRITRDKKGMDRGMYPTYFLHLD-----RED 246
                                                                                                                                                                                                                                                                                                                                                                                                     LNFHGRVTVASVKNFQLVAVSDCEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 437.5; DB 2; Length 460;
Pred. No. 4.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: Nighina, Patsy
APPLICANT: Naggart, Juergen
APPLICANT: No. 6114502en-Trauth, Konrad
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
TITLE OF INVENTION: NEUROSENSORY DEFECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: F8stSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09032365A
Patent No. 6114502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APFILLING DATE:
FILING DATE:
ATTORNES: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
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449 ALSSFDSKLACE 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLSSFETRIACE 380
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  EVQDLEBFALR ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity
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TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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495 ALSSFDSKLACE 506
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Patent No. 5817762
GENERAL INFORMATION:
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DISGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                       247 EVQDLEEFALR------PAPQGITIKCRITRDKKGMDRGMYPTYFLHLD-----RED 292
                                                                                                   293 GKKVFILAGRKRKKSKTSNYLLSVDPTDLSRGGDSYIGKLRSNLMGTKFTVYD----NGV 348
                                                                                                                                                             190 KMQKSRSSNFIKVSPRVPQGSYPIAHISYELAVLGSRGPRRMRCIMDTIP-MSIVESRGV 248
                                                                                                                                                                                    349 NPQXASSSTLESGTLR----QELAAVCYETNVLGFKGPRXMSVI---VPGMNMVHER-- 398
                                                                                                                                                                                                                                           249 VASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWC 308
                                                                                                                                                                                                                                                                                                                                                   GK--FLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAA 189
                                                                                                                                                                                                                                                                       LNFHGRVTVASVKNFQLVAVSDCEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAI 368
EIVAVPEPSSKLTPPISLKQSGPRDSLVQCFIKRNRNTQ-----SYHLYLGLTTSLTDN 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SUSTANTE: BARENIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,553
FILING DATE: 12-ARR-1997
CLLASSIFICATION: S30
PRICK APPLICATION NUMBER: US/08/631,200
FILING DATE: 12-ARR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               369 CLSSFETRIACE 380
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Best Local Similarity 34.9
Matches 109; Conservative
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US-08-829-553-8
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TOPOLOGY:
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Patent No. 5871931
GENERAL INFORMATION:
APPLICANT: Kloyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                          293 GKKVFLLAGRKRKKKSKTSNYLISVDPTDLSRGGDSYIGKLRSNLMGTKFTVYD----NGV 348
                                                                                                                                                                                                                                                                                                                 349 NPQKASSSTLESGTLR-----QELAAVCYETNVLGFKGPRKMSVI----VPGMNMVHER-- 398
                                                                                                                                                                                                                                                                                                                                                                                                ---VSIRPRNEHETILLARWQNK----NTESI------IELQNKTPVWNDDTQSYV 440
                                                                                                                                  78 BIVAVPBPSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQ-----SYHLYLGLTTSLTDN 131
                                                                                                                                                                                                             132 GK--FILAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAA 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                              61;
                                                      Query Match 22.3%; Score 437.5; DB 1; Length 506; Best Local Similarity 34.9%; Pred. No. 5e-40; Matches 109; Conservative 60; Mismatches 82; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,707A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTAZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-100
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212) 790-9090
(212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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amino acid
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495 ALSSFDSKLACE 506
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; MOLECULE TYPE: protein US-08-922-267A-8
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 60
CORRESPONDENS: 60
CORRESPONDENS: Femnie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                 12;
                                                                                                                                                                                                                                                               293 GKKVFLLAGRKRKKSKTSNYLISVDPTDLSRGGDSYIGKLRSNLMGTKFTVYD---NGV 348
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22.3%; Score 437.5; DB 1; Length 506; 34.9%; Pred. No. 5e-40; Live 60; Mismatches 82; Indels 61
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NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 869-9741/8864
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     Query Match
Best Local Similarity 34.9
Matches 109; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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Gaps

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349 NPQKASSSTLESGTLR----QELAAVCYETIVULGFKGPRKMSVI----VPGMNMVHER-- 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 GK--FLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAA 189
                                                                                                                                                                                                                                                                                                                                                                                  190 KMQKSRSSNPIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIP-MSIVESRGV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 VASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWC 308
                                                                                                                               78 EIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQ-----SYHLYLGLTTSLTDN 131
                                                                                                                                                                                                                                                                                         309 LNFHGRVTVASVKNFQLVAVSDCEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAI
                                                                 61;
Length 506;
Query Match 22.3%; Score 437.5; DB 2; Length Best Local Similarity 34.9%; Pred. No. 5e-40; Matches 109; Conservative 60; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 62, Application US/09032365A
; Sequence 62, Application US/09032365A
; Batent No. 6114502
; GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: No. 6114502th, Michael
APPLICANT: No. 6114502th, Michael
APPLICANT: No. 6114502th, Michael
TITLE OF INVENTION: GENE FAMILY ASSOCIATED
ITTLE OF INVENTION: NEUROSENSORY DEFECTS
NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Bozicevic & Reed, Lip
STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEC for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ-2CIP2
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TELECOMMUNICATION INFORMATION
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 506 amino acida
TYPE: amino acida
STRANDEDNESS: single
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495 ALSSFDSKLACE 506
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Sequence 8, Application US/09248203
Sequence 8, Application US/09248203
GENERAL IN- 604346
GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                     78 BIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQ-----SYHLYLGLTTSLTDN 131
                                                                                                                                                                                                                              399 ---VSIRPRNEHETLLARWQNK----NTESI------IELQNKTPVWNDDTQSXV 440
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                                                                                                                                         309 LNFHGRVTVASVKNFQLVAVSDCEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAI
                                          Gaps
                                          61;
             Best Local Similarity 34.9%; Pred. No. 5e-40;
Matches 109; Conservative 60; Mismatches 82; Indels
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1155 Avenue of the Americas
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/936,707
FILING DATE: 24-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-100
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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(212) 869-9741/8864
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STREET: 11
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TELEPHONE:
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                                                                                                                                                                                                                                    61;
                                                                                                                                                         Length 506;
                                                                                                                                                                                                                                82; Indels
                                                                                                                                                     22.3%; Score 437.5; DB 2; 34.9%; Pred. No. 5e-40; live 60; Mismatches 82;
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MEDIUM TYPE: Diskette
COMPUTER: DISKETTE
COMPUTER: DISKETTE
COMPUTER: DISKET DOS
SOFTWARE: PASSESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,824
FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: ADDRESSES: ADDRESSES: Incyte Pharmaceuticals, Inc.
SIREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
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TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                        Best Local Similarity 34.99
Matches 109, Conservative
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495 ALSSFDSKLACE 506
                                       MOLECULE TYPE: protein
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TOPOLOGY: linear
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                                                                          US-09-032-365A-62
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APPLICANT: Kleyn, Patrick W.
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
WUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                           |: : ||: : | 327 EVQDLEEFALR------RED 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 NPQKASSSTLESGTLR----QELAAVCYETNVLGFKGPRKMSVI---VPGMNMVHER-- 398
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATENIN RC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/406,071
                                                                                                                                                                              22.3%; Score 437.5; DB 2; 34.9%; Pred. No. 5e-40; tive 60; Mismatches 82;
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APPLICATION NUMBER: 08/936,707
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-100
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09406071 Patent No. 6207386
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(212) 869-9741/8864
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495 ALSSFDSKLACE 506
                                                                                                                                                                                    Query Match 22.3
Best Local Similarity 34.9
Matches 109; Conservative
                      MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; LIBRARY: GenBark
; CLONE: 1305497
US-08-812-824-4
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linear
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CLASSIFICATION:
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506 amino acids
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                   ; TYPE: amino
; TOPOLOGY: 1
; MOLECULE TYPE:
US-08-955-918C-10
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US-08-697-766A-10
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                        61;
                                                                                                                                                Length 506;
                                                                                                                                                                                       82; Indels
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Patent No. 6268130
GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick, and Moore, Karen
TITLE OF INVENTION: RP Compositions and Therapeutic and
TITLE OF INVENTION: Diagnostic Uses Therefor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DE Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,918C
FILING DATE:
                                                                                                                                                Query Match 22.3%; Score 437.5; DB 2;
Best Local Similarity 34.9%; Pred. No. 5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MNI-007CPDV2CPA TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                       60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILLING JATE AND DATA:
PRIOR APPLICATION NUMBER: US 08/697,766
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: MANDEAGOURAE, AMY E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTER.STICS:
LENGTH: 506 amino acids
TYPE: amino acid
                                                                                                                                                                                   Matches 109; Conservative
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                                                                      TOPOLOGY: unknown // MOLECULE TYPE: protein US-09-406-071-8
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Massachusetts
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US-08-955-918C-10
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293 GKKVFLLAGRKRKKKSKTSNYLLSVDPTDLSRGGDSYIGKLRSNLMGTKFTVYD----NGV 348
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                                                                                                                                                                                                                                                                                               78 BIVAVPEFSSKLTPPISLKQSGPRDSLVQCFIKRNRNTQ-----SYHLYLGLTTSLTDN
                                                                                                                                                                                                      Gaps
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APPLICANT: Gimeno, Carlos; Kleyn, Patrick; and Moore, Karen J.

TITLE OF INVENTION: RP Compositions and Therapeutic and

TITLE OF INVENTION: Diagnostic Uses Therefor

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIUE & COCKFIELD, ILP

STREET: 28 State Street
                                                                                                                                                                                                   61;
                                                                                                                                     Length 506;
                                                                                                                                  Query Match
22.3%; Score 437.5; DB 2; Length EBest Local Similarity 34.9%; Pred. No. 5e-40;
Matches 109; Conservative 60; Mismatches 82; Indels
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ZIP: 05A

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

COMPUTER: 1BM PC compatible

COMPUTER: 1BM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/697,766A

FILING DATE: 29-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08697766A
Patent No. 6399760
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NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-C
TELECOMMUNICATION INFORMATION:
TELEPAX: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 506 amino acida
TYPE: amino acid
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495 ALSSFDSKLACE 506
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: Massachusetts
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us-10-763-042-9.rai

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78 EIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQ-----SYHLYLGLTTSLTDN 131
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                                                                                                                                      |: : ||: : | |: 247 EVQDLEBFALR------RED 292
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                                                                                       61; Gaps
                                                          Query Match 22.3%; Score 437.5; DB 2; Length 506; Best Local Similarity 34.9%; Pred. No. 5e-40; Matches 109; Conservative 60; Mismatches 82; Indels 61.
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495 ALSSFDSKLACE 506
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-697-766A-10
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Search completed: December 23, 2005, 23:29:23
Job time : 48 secs

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Sequence 5, Appli Sequence 19484, A Sequence 254939, Sequence 19510, A

19487, A 19499, A 658, App 612, App

355201, 19488, A 59801, A 307562, 65527, A 128060, 2, Appli 151222,

Sequence

Sequence Seq

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241 SIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NVVACAGVCRSKRILITKEIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELMVLGSRGPRRMRCIMDTIPM
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             US-10-425-114-62614

US-10-425-115-355201

US-10-425-114-59801

US-10-425-114-59801

US-10-425-114-59801

US-10-425-114-6527

US-10-425-114-6527

US-10-425-114-6527

US-10-73-923-19487

US-10-732-923-19487

US-10-732-923-1958

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US-10-732-923-1958
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/10763042

Fublication No. US20050014266A1

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

FILLE OF INVENTION FLANT TUBBY-LIKE PROTEINS

FILLE REFERENCE: 08919-099001

CURRENT APPLICATION NUMBER: US/10/763,042

CURRENT FILING DATE: 2004-01-21

PRIOR APPLICATION NUMBER: US 60/441,380

FRIOR FILING DATE: 2004-01-21

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 380
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; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-763-042-9
RESULT 1
US-10-763-042-9
181
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Sequence 13, Appli
Sequence 184656,
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Sequence 19498, A
Sequence 19499, A
Sequence 57097, A
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Sequence 150007,
Sequence 19497, A
Sequence 19497, A
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Sequence 130, Appl
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Sequence 1, Appli
Sequence 19495, A
Sequence 19496, A
                                                                                                             2005, 23:24:03 ; Search time 163 Seconds (without alignments) 974.081 Million cell updates/sec
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                                                                                                                                                                                                               1 MTFRSLLQEMRSRPHRVVHA......SAFQAFAICLSSFETRIACE 380
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Sequence 11
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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                  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-763-042-11
US-10-763-042-11
US-10-424-599-149493
US-10-424-599-149493
US-10-424-599-284656
US-10-427-963-169301
US-10-425-114-72469
US-10-425-114-72469
US-10-732-923-19480
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US-10-732-923-19495
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                                                                                                                                                                                                                                                                                                  1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 ACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLYLG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ACAGUCRGMRLLAMBTTVVVPEISSKLTFPISLKQPGPRDSLVQCFIKRNRITQSYHLYLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 LITSLIDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 S---QTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIPM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEQLRCWCLNFHGRVTVASVKNFQLVAV-SDCEAG-----QTSERIILQFGKVGKDMFŢ 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 HEQLRCWCLNFHGRVTVASVKNFQLVAAGASCGSGTGMSPERQSERIILQFGKVGKDMFT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 MRSRPHRVVH-----AAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSRRNVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                       72.1%; Score 1414.5; DB 5; Length 72.9%; Pred. No. 7.9e-136; cive 31; Mismatches 51; Indels
                                                                                        Sequence 11, Application US/10763042
Publication No. US20050014266A1
GENERAL INFORMATION:
APPLICANT: Shaw, Joi-Fu
APPLICANT: Lai, Chia-Fing
ITILE OF INVENTION: PLANT TUBBY-LIKE PROTEINS
FILE OF INVENTION: PLANT TUBBY-LIKE PROTEINS
FILE OF ENERGY. 0810-090001
CURRENT APPLICATION NUMBER: US/10/763,042
CURRENT APPLICATION NUMBER: US 60/441,380
FRIOR APPLICATION NUMBER: US 60/441,380
FRIOR FILING DATE: 2004-01-21
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10763042
Publication No. US20050014266A1
GENERAL INFORMATION:
APPLICANT: Shaw , Jei-Fu
APPLICANT: Lai, Chia-Ping
TITLE OF INVENTION: PLANT TUBBY-LIKE PROTEINS
FILE REPERENCE: 08919-09901
CURRENT APPLICATION NUMBER: US/10/763,042
CURRENT FILING DATE: 2004-01-21
FRIOR PILING DATE: 2004-01-21
FRIOR PILING DATE: 2004-01-21
NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                         282; Conservative
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Arabidopsis sp
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                 RESULT 2
US-10-763-042-11
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Best Local S:
Matches 282
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Sequence 149493, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Nongwei
APPLICANT: Cao INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 GSNTY1GKGLRSNFLGTKFTVYDAQPTNPGTQVTRTRSSRLLSLKQVSPR1PSGNYPVAH1 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYELNVLGSRGPRRMRCIMDIIPMSIVESRGV-----VASTSISSFSSRSSPVFRSHSK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 PLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAV-S 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 SYELINVLGSRGPRRMQCVMDAIPASAVEPGGTAPTQTELVHSNLDSFPSFS--FFR--SK 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 RSNAYLGRMRSNFLGTKFTVFDGSQTG-AAKMQKSRSSNFI---KVSPRVPQGSYPIAHI
                                                                                                                                                                                                                                                                                                                                                REILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPR
                                                                                                                                                                                                                                               -RSRPHRVVHAAASTANSSDPFSWSELPEELL
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                               36;
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                                                                                                                                                   Length 406;
                                                                                                                                              58.6%; Score 1149; DB 5; Length 4 56.7%; Pred. No. 1.5e-108; ive 58; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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58.3%; Pred. No. 7.8e-107;
iive 63; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(391)
OTHER INFORMATION: unsure at all Xaa locations
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 149493
LENGTH: 391
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                                                                                                                                            Query Match
Best Local Similarity 56.7
Matches 233; Conservative
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Matches 231, Conservative
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-763-042-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Glycine max
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US-10-424-599-149493
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US-10-43/-y63-193011

US-204-36-193011

Sequence 193011, Application US/10437963

Sequence 193011, Application No. US2040123343A1

GENERAL INPORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Shoukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brand

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 193011

LENGTH 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217
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SNAYLGRARSNFLGTKFTVFDGSQT-GAAKMQKSRSSNFI---KVSPRVPQGSYPIAHIS
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                                                                                                                                                                   353 SE----QAQENVILQFGKVGKDVFTWDYQYPISAFQAFAICLSSFDTKIACE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                             329 SDCEAGQISERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_8918C.1.pep
US-10-437-963-193011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1)..(407)
OTHER INFORMATION: unsure at all Xaa locations
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Matches 221; Conservative
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ORGANISM: Oryza sativa
FEATURE:
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Publication No. US20040031072A1
GENERAL INFORMATION:
BAPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Chou Yihua
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                                                                                                                                                             119 HLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKF 178
                                                                                                                                                                                                   179 TVFDGS--QTGAAKMQKSRSS---NFIKVSPRVPQG-SYPIAHISYELNV-LGSRGPRRM 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 LGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVA-VSDCEAGQTSERIILQF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 IRVETVDGGDWPSRRNVVACAGVCRSWRILIKEIVAVPEFSSKLTFPISLKQSGPRDSLV 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_9906C.1.pep
US-10-424-599-284656
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Matches 232; Conservative
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
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                             APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT PILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 59800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 YELNVLGTRGPRRANCVWHSIPTSCIEAGGTVPSQLDSILARSTDESFGSISFSKSSVVD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 RSHSKPLRSNSASCSD----SGNNLGDP------PLVLSNKAPRWHEQLRCWCLN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 FHGRVTVASVKOFQLVAVSDCEAGQTS-----ERIILQFGKVGKDMFTMDYGYP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDSLVQCFIKRNRNTQSYHLYLGLTTS-LTDNGKFLLAASKLKRATCTDYIISLRSDDIS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 YELMVLGSRGPRRMRCIMDTIPMSIVESRGVVAS------TSISSFS-SRSSPVF 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSFRSIVRDVRDGFGSLSRRGFEVKFLGHRRGRSHGAVHELRDPAPVIOSSCWANLPPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 51.9%; Score 1018; DB 4; Length 436; Best Local Similarity 48.3%; Pred. No. 4.5e-95; Matches 213; Conservative 65; Mismatches 97; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: LIB3591-111-H3_FLI.pep
US-10-425-114-59800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 ISAFQAFAICLSSFETRIACE 380
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ORGANISM: Zea mays
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US-10-425-114-72469
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                                                                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thua
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Brad
APPLICANT: Li, Ping
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APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Sice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 160306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 RSDDISKRSNAYLGRMRSNFLGTKFTVFDG-----SQTGAAKMQKSRSSNFIKVSP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 RVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIPMSIVESRG------VVASTSISS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 FSSRSSPVFRSHSKPLRSNSASCSD-----SGNNLGDP-----PLVLSNKAPRWHE 302
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1 MSFRSIVRDVRDGFGSLSRRGFEVRLVGHRRGRSHSAVHELRDGHAAAAAADVVQSSCWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.2%; Score 1023.5; DB 4; Length 445; 47.6%; Pred. No. 1.3e-95; Live 71; Mismatches 90; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_59597C.1.pep
US-10-437-963-160306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 MFTMDYGYPISAFQAFAICLSSFETRIACE 380
                                                                     Sequence 160306, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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"Sequence 59800, Application US/10425114
"Publication No. US20040034888A1
"GENERAL INFORMATION:
"APPLICANT: Liu, Jingdong
"APPLICANT: Liu, Jingdong
"APPLICANT: Chou, Yihua
"APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTFRSLLQEM-----
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Matches 214; Conservative
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336 SDEEGQNKERPLVLRNKAPRWXHEQLQCWCLNPRGRVTIASVKNFQLIAAXQHRPPAGAP 395
                   244 ESRGVV------ASTSISSFSSRSSPVFRS---HSKPLRSNSASCSDSGNNL 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 QPGPRDATMQCFIKRDKSNLTYHLYLCLSPALLVENGKFLLSAKRIRRTTYTEYVISMHA 179
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                                                                                                    |:||||||| :: |||||| ::|
157 DSGKFLLSAKRHRTTCTEYVISMDADNISRSSTYIGKLRSNFLGTKFIIYDTQPSYNG
                                                                                                                                                             184 SQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIPMSIV
                                                                                                                                                                                  217 AVIPPVXXRSSRRFNSKKVSPKMPSGSYNIAQVTYELMVLGTRGPRRHCVMHSIPASSV
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                                                                                130 DNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRARSNFLGTKFTVFD----G
                                                                                                                                                                                                                                                                     277 RPGGIVPGQPRQIVPRAFEESFRSTTSF-SKSSIMDRSMGFQXFPXDFSSARFSDIAGGT
                                                                                                                                                                                                                                                                                                                             287 GDP-----PLVLSNKAPRW-HEQLRCWCLNFHGRVTVASVKNFQLVAVSDCE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 PEBLLREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 ISSPSSR-----SSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQ
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Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REPERENCE: 38-15(52765)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR PELING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NOS: 24149
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Best Local Similarity 47.1%; Fred. No. 1.4e-94;
Matches 215; Conservative 64; Mismatches 100;
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; ORGANISM: Arabidopsis thaliana
US-10-732-923-19480
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                                                                                                                                                                                                                                                                                      61 LRDVIERLEASE-ATWPNRKSVVSCAAVCRTWREICKEIVKNPEFSGKITFPVSLKQPGP 119
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180 RSSKMYIGKLRSNLLGTKFAIYDTQPPCNAABPGKTSRRFYSRKVSPKVSSSTYNIAQVS 239
                                                                                                                                                                                                                                                                                                                                                                     218 YELNVLGSRGPRRMRCIMDTIPMSIVESRGVVAS------TSISSFS-SRSSPVF 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                 160 KRSNAYLGRMRSNFLGTKFTVFDGSQTGAAKMQKSRSSNF1--KVSPRVPQGSYPIAHIS 217
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1 MSFRSIVRDVRDGFGSLSRRGFEVKFLGHRRGRSHGAVHELRDPAPVIQSSCWANLPPEL
                                                                                                                                                                                                                                                               LREILIRVETVDGGDWPSRRNVVACAGVCRSWRILITKEIVAVPEFSSKLTFPISLKQSGP
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; Publication No. US20050108791A1
; GENERAL INPORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52795)C
; CURRENT APPLICATION NUMBER: US/10/732, 923
; CURRENT FILING DATE: 2003-12-10
; PRIOR PLLING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 19498
; SEQ ID NO 19498
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                                                                                             51.9%; Score 1018; DB 4; Length 436; 48.3%; Pred. No. 4.5e-95; ive 65; Mismatches 97; Indels 6
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              FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-079-H7_FLI.pep
US-10-425-114-72469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(448)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-19498
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Best Local Similarity 48.3
Matches 213; Conservative
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 206; Conserv
ORGANISM: Zea mays
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US-10-732-923-19498
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Gaps

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Query Match
Best Local Similarity 48.04
Matches 212; Conservative
                                                                                                                                                   ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 DNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGS--QTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 SRGVV------ASTSISSFSSRSSPVFRS--HSKPLRSNSASCSD----- 281
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11 RSRPHRVVHAAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSRRNVVACAGVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                               Sequence 41195, Application US/10767701
; Sequence 41195, Application No. US20040172684A1
; GENERAL INFORMATION:
APPLICANT: Exou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Ass
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Ass
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Ass
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Ass
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Ass
; TITLE OF INVENTION: Nucleic Acid Molecules Ass
; CURRENT PRILIGO DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
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                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: SORBI-28MAY03-C27_1.pep
                                            GKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE 380
                                                            420 GKVGKDMFTMDFRYPLSAFQAFAICLSSFDTKLACE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.5%; Score 1011; DB 4;
50.2%; Pred. No. 2.5e-94;
tive 65; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57097, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.29
Matches 209; Conservative
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US-10-425-114-57097
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US-10-767-701-41195
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REPRENCE: 38-21(53313)B; CURRENT APPLICATION UNDER: US/10/425,114; CURRENT FILING DATE: 2003-04-28; NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 57097
LENGTH: 437
TYPE: nor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 YELNVIGSRGPRRMRCIMDTIPMSIVESRGVVAS------TSISSFS-SRSSPVF 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 LREILIRVETVDGGDWPSRRNVVACAGVCRSWRILIKEIVAVPEFSSKLTFPISLKQSGP 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 KRSNAYLGRMRSNPLGTKFTVFDGSQTGAAKMQKSRSSNF1--KVSPRVPQGSYPIAHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RSRPHRVVHAAASTANSSDPFSWSELPEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.5%; Score 1010.5; DB 4; Length 437; 48.0%; Pred. No. 2.6e-94; ive 66; Mismatches 97; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: LIB4572-001-D3_FLI.pep
US-10-425-114-57097
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SCANIEN: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_116208C.1.pep
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US-10-425-115-202431
Sequence 202431, Application US/10425115
Sequence 202431, Application US/10425115
Sequence 202431, Application US/10425115
Sequence 202431, Application US/10425115
Set Deblication No. US2004021427241
APPLICANT: La Rosa Thomas J.
APPLICANT: Application Acid Molecules and TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 202431
LENGTH: 437
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DNGKFILLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFD--GSQTG 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 SRGVV------ASTSISSFSSRSSPVFRS--HSKPLRSNSASCSD-----S 282
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                                                                                                                                                                                                                                          156 DSGKFLLSAKRHRKTTCTEYVISMDADNISRSSSTYIGKLRSNFLGTKFIIYDTQPSYNG
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Job time : 165 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LRDVIERLEASE-ATWPNRKSVVSCAAVCRTWREICKEIVKNPEFSGKITFPVSLKQPGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDSLVQCFIKRNRNTQSYHLYLGLTTS-LTDNGKFLLAASKLKRATCTDYIISLRSDDIS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRSNAYLGRMRSNFLGTKFTVFDGSQTGAAKMQKSRSSNF1--KVSPRVPQGSYPIAHIS 217
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180 RSSKMYIGKLRSNLLGTKFAIYDTQPPCNAABPGKTSRRFYSRKVSPKVSSSTYNIAQVS 239
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1 MSFRSIVRDVRDGFGSLSRRGFEVKFLGHRRGRSHGAVHELRDPAPVIQSSCWANLPPEL
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                                                                               DB 4; Length 437;
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                                                                       51.5%; Score 1010.5; DB 4; Length 48.0%; Pred. No. 2.6e-94; ive 66; Mismatches 97; Indels
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US-10-437-963-150007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PISAFOAFAICLSSFETRIACE 380
                                                                       Query Match 51.5
Best Local Similarity 48.0
Matches 212; Conservative
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                                                                                                                                                                                                                                      MTFRSLLQEM-
US-10-425-115-202431
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US-10-437-963-150007
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 23, 2005, 23:12:06 ; Search time 39 Seconds
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Run on: December 23, 2005, 23:12:06; Search time 39 Seconds (without alignments) 937.497 Million cell updates/sec Title: US-10-763-042-9 Perfect score: 1962 Sequence: 1 MTFRSILQEMRSRPHRVVHA......SAFQAFAICLSSFETRIACE 380

Sequence: 1 MTFRSLLQEMRSRPHRVVHA...
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	- ;	H84920	H96797	E86382	E96513	E84562	F96499	S42728	S68518	T20691	T02138	E86295	B86347	D84634	H85068	H85063	T48957	T12064	S57180	149350	H96795	F96671	S71792	S45859	S64030	T52569	H86319	G86342	ın	JC5957
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ALIGNMENTS

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	Query Ma Best Loc Matches	Query'Match 58.5%; Score 1147.5; DB 2; Length 407; Best Local Similarity 56.6%; Pred. No. 5.6e-92; Matches 233; Conservative 57; Mismatches 85; Indels 37; Gaps 9;	
	ඊ සි	1 MTFRSLLQEM	
	& B	42 REILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPR 101 :: : :	
-	& 8	102 DSLVQCFIKRNRNTQSYHLXILGLTTSLTDNGKFLLAASKLKRATCTDXIISLRSDDIS 159	
	& 8	160 KRSNAYLGRMRSNFLGTKFTVFDGSQTG-AAKMQKSRSSNF1KVSPRVPQGSYPIAH 215:	
	& 8	216 ISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHS 269	
	& 43	270 KPLRSNSASCSDSGNNLGDPPLVLSNKAPKWHEOLRCWCLNFHGRYTVASVKNFOLVAV- 328 : :	

원 장

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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudhes, B.; Hudzar, L.
Nature 408, 816-820, 2000.
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzaberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Reference number: A86141; MuID:21016719; PMID:11130712
A,Residues: preliminary
A,Molecule type: DNA
A,Residues: 1-445 <SIO>
A,Gooss-references: UNIPROT:Q9FRH7; UNIPARC:UPI0000A1436; GB:AE005172; NID:g11067277; PJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                         50.9%; Score 999.5; DB 2; 47.2%; Pred. No. 4.9e-79; ive 71; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                         C,Genetics:
A,Map position: 1
C,Superfamily: F-box protein tubby-like, plant type
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Best Local Similarity 47.2
Matches 212; Conservative
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                                                                                                        hypothetical protein F22K20.1 [imported] - Arabidopsis thaliana Gispecies: Arabidopsis thaliana (mouse-ear cress)
Gispecies: Arabidopsis thaliana (mouse-ear cress)
Gispecies: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
Gispeciession: H96797
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.G., Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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               ENGPAGPEHENVILQFGKVGKDVFTMDYQYPISAFQAFTICLSSFDTKIACE
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A; Residues: 1-455 <STO>
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Length 445;

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C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Aracession: B. Sebsia
R. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; A.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chi, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A. Authors: Hunter, J. Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. A. Authors: Salzbergy S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. A.; Wu, D.; Yu, G.; Praser, C.M.; Vonter, J.C.; Davis, R.W.
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLR 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 FRSNISFSKSSFDHRSLDFSSSRFSEM---GISCDDNEEBASFRPLILKAKQPRWHBQLQ 356
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                                                                                                                                                                                                                               LKOSGPRDSLVQCFIKRNRNTQSYHLYLGLTTS-LTDNGKFLLAASKLKRATCTDYIISL 153
                                                                                                                                                                                                                                                                                                                                                                                RSDDISKRSNAYLGRMRSNFLGTKFTVFD-----GSQTGAAKMQKSRSSNF--IKVSPRV 206
9
                                                                          94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWCLNFHGRVTVASVKNFQLVAV----SDCEAGOTS-----ERIILOFGKVGKDM
                                                                      ELPEELLREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POGSYPIAHISYBLNVLGSRGPRRMRCIMDTIPMSIVESRGVV-----
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hypothetical protein T10P12.9 [imported] - Arabidopsis thaliana
hypothetical protein T10P12.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear crees)
C;Boscies: Arabidopsis thaliana (mouse-ear crees)
C;Boscies: Down-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C;Accession: P96499
C;Accession: P96499
Chin, C. M.; Ari Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R;Theologis, A.; Ecker, J.R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizaco, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
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                              46 IRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPRDSLV
                                                       166 LGRMRSNFLGTKFTVFDG-SQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLG
                                                                                                                                                                                                                                                                                                                                              225 SRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFR--SHSKPLRSNSASCSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEAG---QTSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 TPPISLKQSGPRDSLVQCFIKRNRNTQSYHLYLGLTTS-LTDNGKFLLAASKLKRATCTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 IILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE 380
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40.1%; Score 787.5; DB 2;
Best Local Similarity 43.2%; Pred. No. 1.3e-60;
Matches 168; Conservative 65; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Gene: T10P12.9
:Map position: 1
;Superfamily: F-box protein tubby-like, plant type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-415 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C;Accession: E84562
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Macrman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Mature 402, 761-768, 1999
MyTitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; WUID:20083487; PMID:10617197
A;Accession: E84562
A;Accession: E84562
A;Accession: E9650
A;Accession: Landinary
A;Residues: 1-386 <STO>
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                        A;Accession: E96513
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-388 <STO>
A;Cross-references: UNIPROT:Q9C6B4; UNIPARC:UPI0000A18D9; GB:AE005173; NID:g10092408;
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 PPPFNRKLPPS-----MQVSPWVSSSSSSYNIASILYELNVLRTRGPRRMQCIMHSIPIS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 TSLT-DNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEAG-----QTSERIILQFGKVGKDMF 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 QTG-AAKMQKSRSSNFIKVSPRV--PQGSYPIAHISYELNVLGSRGPRRWRCIMDTIPMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 IVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDS--GNNLGDPPLVLSNKAPR
                                                                                                                                                                                                                                                                                                                                                                                                  11 RSRPH-----RVVHAAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSRRNVVAC
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                                                                                                                                                                                                                                                                                       Length 388;
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                                                                                                                                                                                                                                                                                                                                              92; Indels
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
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49.4%; Pred. No. 3.7e-72;
ive 59; Mismatches 107;
                                                                                                                                                                                                                                                                                    Query Match 47.3%; Score 929; DB 2; Best Local Similarity 50.8%; Pred. No. 5.5e-73; Matches 197; Conservative 65; Mismatches 92.
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C,Superfamily: F-box protein tubby-like, plant type
                                                                                                                                                                              A;Gene: P8G22.1
A;Map position: 1
C;Superfamily: F-box protein tubby-like, plant type
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Matches 198; Conservative
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A;Map position: ?
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A, Experimental source: clone F10B5 C; Genetics:
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Best Local Similarity 28.13
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||::::|||
494 ALSSFDSKLACE 505
                                                                                            Query Match
Best Local Similarity 33.7
Matches 105; Conservative
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A Cross-references: UNIPARC:UPI0000161D82; EMBL:X69827; NID:g467577; PIDN:CAA49481.1; PI
A;Notes: the sequence of residues 177-215 and the corresponding nucleic acid sequence are
C;Superfamily: tubby
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                                                                                                                                                                                                                                                                                          phosphodiesterase (clone p4-6) - mouse
phosphodiesterase (clone p4-6) - mouse
C;Species: Mus musculus (house mouse)
C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2004
C;Accession: S42728; 148711
R;Vambutas; V.; Wolgemuth, D.J.
Biochim Biophyse. Act 1217, 203-206, 1994
A;Title: Identification and characterization of the developmentally regulated pattern carried and characterization of the mounder: 148711; MUID:94153998; PMID:7509194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-505 <NOB>
A;Residues: 1-505 <NOB>
A;Accession: S68519
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153
                    267 EFLORSLDESFRSIGSSKIVNHSGDFTRPKEBEGKVRPLVLKTKPPRWLQPLRCWCLNFK 326
                                                                           351
                                                                                                  154 RSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AHISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------LPGMDSRKO---RMKVOPON 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 SNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 DODSILSRVOKGAGHGLLLLONKAPSWSDESGAYVINFHGRVSRASVKNFQIVHPDE--- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tub protein, brain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Apte: 15-Nov-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C;Accession: $68518; $68519
R;Noben-Trauth, K:; Naggert, J.K.; North, M.A.; Nishina, P.M.
Nature 380, 534-538, 1996
A;Title: A candidate gene for the mouse mutation tubby.
A;Reference number: $68518; WUID:96195061; PMID:8606774
A;Accession: $68518
A;Efetus: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 PRDHMVQWRIVRNKHGMDKGMPPSYYLYLEGEDGV---AHFLLAGRKRKRSKTSNYLISL
                                                                             ---ERIILOFGKVGKDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 PRDSLVQCFIKRNRNTQ----SYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.3%; Score 437.5; DB 2; Length 271; 36.6%; Pred. No. 2e-30; Live 45; Mismatches 90; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 GQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::||||:| ::||||: ---PDHIVLQFGRVAPNIFTMDFRYPLCPLQAFAICLSSFDGKLACE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Mismatches
                                                                                                                                                                               387 FIMDYRYPLSAFQAFAISLSTFDTKLACE 415
                                                                                                                                                             FIMDYGYPISAFOAFAICLSSFETRIACE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S42728
A; Status: nucleic acid sequence not shown
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VFRSHSKPLRSNSASCSDSGNNLGD
                                                                             GRUTVASVKNPQLVAVSDCEAGQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 36.6
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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                                                                             313
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A;Residues: 47-505 <NO2>
A;Cross-references: UNIPARC:UP100001488EE; EMBL:U52824; NID:g1280436; PIDN:AAC52512.1; P)
C;Superfamily: tubby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reaidues: 1-425 <WIL>
A;Cross-references: UNIPARC:UP1000017BBD2; EMBL:Z48334; PIDN:CAA8B311.1; GSPDB:GN00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 RN-----TQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 GRMRSNFLGTKFTVPDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSR 226
                                                                                                                                                                                                     131
                                                                                                                                                                                                                                                                                                                                                                                                                                        249 VASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSCNNLGDPPLVLSNKAPRWHEQLRCWC 308
                                                                                                                                                                                                                                                                                                       132 GK--FILLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F10B5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T20691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : || : : |: |: |: || : | || : || || 60 TQDPIAQPRWGSMPRQQPQQ-VQESLISI-----GDYPDNDINAKLSKVNLTSCVVSDDE
                                                                                                                                                                                                                                                                                                                                 I-------RPRNEHETLLARWQNKNTESIIELQNKTPVWNDDTQSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 INFHGRVTVASVKNPOLVAVSDCBAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 EIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQ-----SYHLYLGLTTSLTDN
                                                                                                                                                                                                                                     246 BVQDLEBFALR------PAPQGITIKCRITRDKKGMDRGMYPTYFLHLD-----RED
                                                                                                                                                                                                                                                                                                                                                                                                           190 KMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIP-MSIVBSRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                      61;
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                                                                                                    Length 505
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                                                                                                                                                      Indels
                                                                                                    22.2%; Score 436.5; DB 2; 33.7%; Pred. No. 6e-30; ive 60; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.1%; Score 394.5; DB 2; 28.1%; Pred. No. 2.1e-26; iive 74; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 SSDPFSWSEL-----PEELLREILIRVETVDGGDWP.
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A;Accession: T20691
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: T20691
R,Sims, M.
submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 2
A;Introns: 28/2; 85/2; 151/2; 269/3; 337/1; 407/1
C;Superfamily: tubby
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ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.L.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M., D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: B86295
A; Accession: B86295
A; Accession: Recognitionary
A; Mesidues: preliminary
A; Mesidues: preliminary
A; Mesidues: A. STOS
                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:Q9S9M8; UNIPARC:UPI00000AAF61; GB:AE005172; NID:g6587813; PII
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 QS-----YHLY------LGLTTSLTDNGKFLL-AASKLKRATCTDYIISLRSDD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 ISKRSNAYLGRMRSNFLGTKFTVFD-GSQTGA-AKMQKSRSSNFIKVSPRVP--QGSYPI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 RSWRILTKE---IVAVPEFSSKLTFPISLKQSGPRDSLV------QCFIKRNRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.2%; Score 201; DB 2; Length 397; Best Local Similarity 24.4%; Pred. No. 1.4e-09; Matches 87; Conservative 54; Mismatches 103; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Vysotskala, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.; Li rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.
A;Reference number: 214574
                                                        GPRRAMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNL 286
                                                                                                                                                 287 GDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEAGQTSERIILQFGK 346
                                                                                                                                                                              321 LDSLKILSNKSPQWNDETQSYVLNFHGRVTQASVKNFQIIHQS-----SPEYIVWQFGR 374
         231 AKVRSNALGTQFTVYDSGQ-----NPKKTTNHAAIRQE-----LAAVIYETNVLGFK 277
                                                                                                    278 GPRKWTIVMP-----GIEPPT----ENRPAVRCPVRPIODKHTLLERYRLND 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 KOSGPRDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 DDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 ISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSN 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 SASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLLNFHG-RVTVASVKNFQLVAVSDCEAG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SGQKEG--VLVLKSKVPRLEEQ--SWCLDFNGWRDIVSSGKKFQLVALL---- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTSERIILQFGKVGKDMFTMDYGY----PISAFQAFA----IC----LSSFETRIA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F8K4.13 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 LPEELLREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 5e-23;
---rhes 76; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 VGKDMFTMDYGYPISAFQAFAICLSSFETRIA 378
                                                                                                                                                                                                                                                                         375 ISDDEFTMDFRYPLSAVQAFGIAMTSFHGKLA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.0%; Scc. No. 5c. 29.3%; Pred. No. 5c. ... 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T02138
A; Status: translated from GB/EMBL/DDBJ
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A;Introns: 61/3; 110/1; 199/3
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Best Local Similarity
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A; Residues: 1-265 < VYS>
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                                                        227
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Proportetical protein F24J8.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86347
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anter 408, 816-820, 2000 Universe and ansen, N.F.; Hudbes, B.; Huizar, L.
Nature 408, 816-820, 2000 Universe ansen, N.F.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, C.M.; Venter, J.C.; Davis, R.W.
A;Hile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: Assell41; MUID:21016719; PMID:11130712
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214 AHISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 SNSASCSDSGNNLGDPPLVLS----NKAPRWHEQLRCWCLNF--HGRVTV---ASVKNF 323
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

hypothetical protein T24D18.17 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004

C; Accession: E86295

Gaps

54;

57 63 66

211

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C;Accession: H85068
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Itle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Accession: H85068
A;Cetsion: H85068
A;Cetsion: H85068
A;Cetsion: Preliminary
A;Accession: H85068
A;Accession: H85068
A;Accession: H85068
A;Cetsion: Preliminary
A;Residues: 1-322 <STO>
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprinc Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85063
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                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:Q9M0U7; UNIPARC:UPI0000A04CC; GB:NC_001268; NID:g7267308; P1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ARK-----LCRAWRRICKDPSMWRKINLRDCLMYBFDFESMCRHIVDLSQGGLLBINI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 ---PRDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein AT4905080 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---DISKRSNA--YLGRMRSNFLGTKFTVFDGSQTGAAKMQKSRSSNFIKVSPRVPQGSY
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Pred. No. 0.34;
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C,Superfamily: F-box containing protein
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nes 62; Conservative
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A;Molecule type: DNA
A;Residues: 1-391 <STO>
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Best Local S:
Matches 56
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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A;Residues: 1-695 <STO>
A;Cross-references: UNIPROT:Q9ZUHO; UNIPARC:UPI000017A78D; GB:AE002093; NID:g4115385;
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                                                                                                                                                                                                                                                                                       78 ---EIVAVPEFSSKLTFPISLKQSGPR--DSLVQCFIKRNRNTQSYHLYLGLTTSLTDNG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                    28 WKDIPVELLMRILSLVDD------RNVIVASGVCTGWRDAISFGLTRLRKGWNNM
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                                                                                                                                                       33 WSELPEELLREILIRVETVDGGDWPSRRNVVACAGVCRSWRI----LTK--
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20.4%; Pred. No. 0.5;
:ive 52; Mismatches 153;
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N7-like protein [imported] - Arabidopsis thaliana
                                                       ; Pred. No. 0.11; 21; Mismatches
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                                                       ilarity 26.7%;
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Best Local Similarity 20.49
Matches 81; Conservative
                                                   Best Local Similarity
Matches 43; Conserv
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A; Status: preliminary
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Search completed: December 23, 2005, 23:28:33 Job time : 43 secs

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FUBLICATION NO. US20050014266A1
GENERAL INFORMATION:
APPLICANT: Shaw, Jei-Fu
APPLICANT: Lai, Chia-Ping
TITLE NOF INVENTION: PLANT TUBBY-LIKE PROTEIN:
FILE REFERENCE: 08919-099001
CURRENT APPLICATION NUMBER: US/10/763,042
CURRENT PILING DATE: 2004-01-21
RIOR APPLICATION NUMBER: US 60/441,380
FRIOR APPLICATION NUMBER: US 60/441,380
FRIOR PRING DATE: 2004-01-21
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 1140
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100.0%; Pred. No. 0;
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Best Local Similarity 100.
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 RESULT 1
US-10-763-042-20
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Sequence 216, App
Sequence 19528, A
Sequence 19311, A
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Sequence 11315,
Sequence 117, Appl
Sequence 17, Appl
Sequence 105685,
Sequence 21, Appl
Sequence 129, Appl
Sequence 129, Appl
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                                                                            03:28:09; Search time 1104 Seconds (without alignments) 8539.032 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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Compugen Ltd.
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US-10-763-042-22
US-00-425-114-8367
US-10-425-114-8367
US-10-424-599-6651
US-10-424-599-6651
US-10-424-599-14814
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US-10-424-599-14814
US-10-424-16
US-10-425-114-19311
US-10-425-114-19311
US-10-425-115-119315
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US-10-763-042-17
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US-10-763-042-17
US-10-225-068-129
US-10-225-068-129
US-10-744-599-64212
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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              GenCore version (c) 1993 - 2005
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Maximum Match 100%
Libting first 45 summaries
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Gaps

51;

Length 1140; Indels 117 108 168 237 228 297 348 417

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CTGCTTAGAGAAATCCTGATTAGGGTTGAGACTGTTGACGGCGGCGATTGGCCGTCGCGG 177
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                                      Score 567.8; DB 8;
Pred. No. 6.9e-183;
0; Mismatches 252;
                                     49.8%;
al Similarity 72.8%;
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         , ORGANISM: Arabidopsis
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                                       Query Match
Best Local S
Matches 810
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TATCTCGGATTAACTACTCTTTGACGGATAACGGGAAGTTTCTTCTTGCTGCTTCTAAG
                                        CATGAGCAGTTACGTTGCTGGTGCTTAAATTTCCATGGTCGAGTCACAGTGGCTTCGGTT
                                                                      CTGAAGCGCGCAACTTGCACTGATTACATCATCTCTTTGCGTTCAGACGATATCTCAAAG
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Publication No. US20050014266A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: PLANT TUBBY-LIKE PROTEINS
FILE REFERENCE: 08919-099001
CURRENT APPLICATION NUMBER: US/10/763,042
CURRENT FILING DATE: 2004-01-21
FRIOR APPLICATION NUMBER: US 60/441,380
FRIOR FILING DATE: 2004-01-21
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 1140
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                                                 ACABTACCTATGAGGATCGTGGAGGAGGAGTAGTAGCTTCAAAGCTCT
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APPLICANT: Libu, Jingdong
APPLICANT: About Xibua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
TYPE. no.-
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                                                                       301 CGTTCAGACGATATCTCAAAGAGAAGCAACGCGTATCTTGGGAGAATGAGATCGAACTTC
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Pred. No. 3.2e-114;
0; Mismatches 367;
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Best Local Similarity 63.2%;
Matches 674; Conservative (
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ORGANISM: Glycine max
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988 GGAATGTCACCGGGGGAGAGCGAGAGCGGGTTATATTGCAGTTTGGGAAAGTCGGGAAA 1047
                                                                                             1048 GATATICTACCATGGATTATGGATACCCGATCTCAGCTTTCCAGGCTTTTGCCATTTGC 1107
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                                                             1048 GACATGTTTACCATGGATTATGGATATCCGATTTCTGCGTTTCAAGCGTTTGCTATCTGC
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34.7%; Score 396; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 3e-124;
Matches 396; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2028 (PARA-017PRV)
CURRENT APPLICATION NUMBER: US/09/770,423
CURRENT FILING DATE: 2001-01-26
PRIOR PILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FRASESQ for Windows Version 4.0
                                                                                                                                                               1108 TTGAGCAGCTTTGAGACTAGAATCGCTTGTGAA 1140
                                                                                                                                      1108 CTGAGCAGTTTTGAAACCAGAATTGCCTGTGAA 1140
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Publication No. US20020040490A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joshua G.
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Allen, Keith
Hoffman, Neil
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Slader, Ted
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LENGTH: 396
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444 CCGAGGACACGTGGCCGCCGCGGAAGAGCGTCGTCTCCTGCGCCGCGGCGTCTGCCGCAGCT
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                                GGAGGATTCTCACCAAGGAGATTGTAGCTGTTCCTGAATTCTCCTCTAAATTGACTTTCC
                                                           GGAGACATATCACCAÁAGACATTGTCAAAACGCCCGAACTCTCCTCCAAGATCACCTTCC
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Publication No. US20050014266A1
GENERAL INFORMATION:
APPLICANT: Shaw , Jei-Fu
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US-10-763-042-14
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US-10-424-599-6651
US-10-424-599-6651
Sequence 6651, Application US/10424599
Publication No. US2004003107241
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: APPLICANT: A CO YONGWei
TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5322)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PRIJNG DATE: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                    1111 GAAAAGTTGGGAAGGATTTGTTTACAATGGATTACCGGTACCCTATCTCGGCATTTCAGG 1170
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CGAGAAGAATGCGTTGCATCATGGATACAATACCTATGAGCATCGTGGAGTCGCGAGGAG
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                                                                                                                                                                                                                                       803 ACTCAAAACCATTGCGCAGTAATAGTGCATCATGTAGCGACTCAGG-----CAACAACC
                                                AGGGAAGTTACCCCATCGCTCACATTTCATACGAGTTAAACGTCTTAGGCTCTCGGGGAAC
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Pred. No. 3.2e-107;
0; Mismatches 364;
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30.5%;
Best Local Similarity 63.2%;
Matches 676; Conservative
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APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 141814
                                                                                                                                        719 ATCGCAGTAATCAAACATATTATCTTGTTTTTTTTAAACCAAGCCTCAACTGATGAAG
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     TCTCCTTCTTCAGGTCGAAATCAATTCGTGCAGAGAGTCTCCCTTCTGGTCCATCATCTG
                                                                             926 crecrcadaaggaaggacrecritarercridaaaaacaaagcgcccagarggcacgaacagc
                                                                                                                                                                                           971 AGCTTGTGGCAGTTAGTGACTGTGAA---GCAGGGCAGACATCTGAGAGGATCATACTCC
                                                                                                                                                                                                                                 1046 AGCTGGTAGCTGCTCGTGAGAATGGACCTGCAGGACCTGAGCACGAAAACGTGATTCTCC
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                                           851 ACAACCTGGGAGATCCACCATTGGTGCTGAGCAACAAAGCTCCACGGTGGCATGAGCAGT
                                                                                                                    TACGTTGCTGGTGCTTAAATTTCCATGGTCGAGTCACAGTGGCTTCGGTTAAGAACTTTC
                                                                                                                                                                                                                                                                                          95 GCTGGTCGGAGCTCCCGGAGGAGCTGCTTAGAGAAATCCTGATTAGGGTTGAGACTGTTG
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Pred. No. 7.6e-105;
0; Mismatches 389;
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US-10-424-599-141814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 141814, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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Best Local Similarity 61.0%;
Matches 651; Conservative
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APPLICANT: Kovalic David K
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US-10-424-599-141814
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Pred. No. 1.2e-105;
0; Mismatches 429;
APPLICANT: Lai, Chia-Ping
TITLE OF INVENTION: PLANT TUBBY-LIKE PROTEINS
FILE REFERENCE: 08919-099001
CURRENT APPLICATION NUMBER: US/10/763,042
CURRENT FILING DATE: 2004-01-21
PRIOR PLILING DATE: 2004-01-21
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 1218
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30.1%;
Best Local Similarity 59.8%;
Matches 677; Conservative
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; ORGANISM: Arabidopsis sp.
US-10-763-042-14
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                                                          839 cicraaacrengardarerateaagagagagragraecrararregaaagrigagareaa 898
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CTTTGCGTTCAGACGATATCTCAAAGAGAAGCAACGCGTATCTTGGGAGAATGAGATCGA
                                                                                                                                515 ACTICCTIGGAACAAATICACGGICTTIGAIG------GIAGICAGACCGGAG
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US-09-770-444-216/c
Sequence 216, Application US/09770444
; Sequence 106, Application US/09770444
; Patent No. US20020023280Al
; GENERAL INFORMATION:
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Rameaka, Joshua G.
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Kricker, Maja
Slader, Ted
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Davis, Keith R. Allen, Keith Hoffman, Neil

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Sequence 90528, Application US/10437963
; Sequence 90528, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Planta and Uses Thereof for Plant Improvement
; TILLE OF INVENTION: Planta and Uses Thereof for Plant Improvement
; TILLE OF INVENTION: Planta and Uses Thereof for Plant Improvement
; TILLE OF INVENTION: UNMBER: 105/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 90528
; LENGTH: 1910
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                                                                                                                                                                                                                                                                                                                                                                                    Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
TITLE OF INVENTION: Expressed Sequences of Arabidopsis TITLE OF INVENTION: thaliana FILE REFERENCE: 2027 (PARA-016PRV) CURRENT APPLICATION NUMBER: US/09/770,444 CURRENT FILING DATE: 2001-01-26 PRIOR PELING DATE: 2000-01-27 NUMBER OF SEQ ID NOS: 999 SOFTWARE: PastSEQ for Windows Version 4.0 LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                  28.6%; Score 326; DB 3; Le
ilarity 100.0%; Pred. No. 3.3e-100;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-216
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Best Local Similarity
Matches 326; Conserv
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319 ATCTCATTGAAACAGCCGGGCCTCGAGACTCTCCAATTCAATGTTTTAAGAGGAAC 378
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Pred. No. 4.8e-74;
0; Mismatches 441;
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TITLE OF INVENTION: Chia-Fing
FILE REFERENCE: 08919-099001
CURRENT APPLICATION NUMBER: US/10/763,042
CURRENT FILING DATE: 2004-01-21
PRIOR PILING DATE: 2004-01-21
PRIOR PILING DATE: 2004-01-21
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 13
         1859 TCAATCATTTGCAATCTGTCTGAG 1882
                                                                                                                                                  Sequence 13, Application US/10763042
Publication No. US20050014266A1
GENERAL INFORMATION:
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al Similarity 55.4%;
585; Conservative
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; ORGANISM: Arabidopsis sp.
US-10-763-042-13
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Best Local Similarity
Matches 585; Conserv
                                                                                           RESULT 10
US-10-763-042-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1182
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Sequence 112097, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: A cost Thomas J

TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE REFERENCE: 38-21(53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 112097

LENGTH: 1939
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                                                                                        AGTTAAACGTCTTAGGCTCTCGGGGACCGAGAAGAATGCGTTGCATCATGGATACAATAC
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Pred. No. 1.9e-66;
0; Mismatches 424;
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US-10-424-599-112097
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ORGANISM: Glycine max
FEATURE:
NAME.Y. unsure
LOCATION: (1)..(1939)
OTHER INFORMATION: unsure at all n locations
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Best Local Similarity 54.4%;
Matches 552; Conservative (
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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------CTTAAGGGACCAACCGCTA 903
                                                                                                                                                                                           904 GITCICAAAAACAAATCCCCAAGAIGGCAIGAGCAGIIGCAGGGGCTGCTCAACIIC 963
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                                                                                                                                                       GTGCTGAGCAACAAAGCTCCACGGTGGCATGAGCAGTTACGTTGCTGGTGCTTAAATTTTC
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Pred. No. 8.1e-67;
0; Mismatches 298;
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US-10-425-114-19311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19311, Application US/10425114
; Publication No. US20040034888A1
; GENEAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                            859 AAAGAGATTCCTGATAATTCTCCAAG-
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Best Local Similarity
Matches 472; Conserv
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US-10-425-114-19311
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Pred. No. 1.4e-63;
0; Mismatches 411;
                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: MRT4577_40299C.1
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FITLE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 119115
LENGTH: 2358
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Best Local Similarity 55.2%;
Matches 562; Conservative (
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US-10-425-115-119315
; Sequence 119315, App.
; Publication No. US20
; GENERAL INFORMATION:
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Sequence 119315, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:

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56.0%;
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Best Local Similarity 56.0
Matches 593; Conservative
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US-10-424-599-8380
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Sequence 12426, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53835)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 12426
LENGTH: 1183
                                                       GCTTGTGGCAGTTAGTGACTGTGAAGCAGGCAGACATCT-----GAGAGGATCAT 1022
                                                                                                                 1023 ACTCCAGTTTGGGAAAGTTGGGAAGGACATGTTTACCATGGATTATGGATATCCGATTTC 1082
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US-10-767-701-12426
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Best Local Similarity 62.3%;
Matches 454; Conservative
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US-10-767-701-12426
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Sequence 8380, Application US/10424599
; Sequence 8380, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: La Rovalic David K
    APPLICANT: Zhou Yihua
    APPLICANT: Cao Yongwei
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REFERENCE: 38-21 (5322)B
    CURRENT APPLICATION NUMBER: US/10/424,599
    CURRENT FILING DATE: 2003-04-28
    NUMBER OF SEQ ID NOS: 285684
    SEQ ID NO 8380
    LENGTH: 2451
                                                                                                                                                                                                                                                                                                                                                                                                                   TATCCGATTTCTGCGTTTCAAGCGTTTGCTATCTGCCTGAGCAGTTTTGAAACCAGAATT 1131
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Pred. No. 2.3e-63;
0; Mismatches 382;
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US-10-424-599-8380
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949 GTGGCTTCGGTTAAGAACTTTCAGCTTGTGGCAGTTAGTGACTGTGAAGCAGGGCAGACA 1008
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912 GCTGACAACATCTCTAGATCCAGTAACACTTACATTGGAAAGCTGAGATCAAATTTTCTT 971
                         523 GGAACAAATTCACGGT---------CTTTGATGGTAGTCAGACCGGA 561
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GenCore versi Copyright (c) 1993 - 200 OM nucleic - nucleic search, using sw mode Run on: December 26, 2005, 01:49:0 Fitle: US-10-763-042-20 Perfect score: 1140 Sequence: 1 atgacgttccgaagtttact Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0 Searched: 41078325 seqs, 23393541228 Total number of hits satisfying chosen par Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 10% Listing first 45 summaries Listing first 45 summaries Listing first 45 summaries EST:* 1: 9b_est1:* 2: 9b_est2:* 3: 9b_est2:* 4: 9b_htc:* 5: 9b_est3:* 7: 9b_est5:* 7: 9b_est6:* 8: 9c_est5:* 11: 9b_gss1:* 10: 9b_gss1:* 11: 9b_gss2:* 11: 9b_gss2:* 11: 9b_gss2:* 11: 9b_gss2:* 11: 9b_gss3:* 1	Query Duely Length DB ID ID ID ID ID ID ID ID ID ID ID ID ID

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BX822204.1 GI:42463850
HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1261)
Menard, M., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission

Loud Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

By 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
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/tissue_type="Flowers and
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/mol_type="mRNA"
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/gene="At3g06380"
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2 (bases 1 to 1261)
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- Web: www.genoscope.cns.fr)

The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH44ZH11 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress). Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta, Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1535)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Craud,C., Quetiar,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome 'n Direct Submission Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (8-mail : segref@genoscope.cns.fr 259 GCCGCCTCAACCGCTAATAGTTCAGACCCTTTCAGCTGGTCGGAGCTCCCGGAGGAGGTG 120 121 CTTAGAGAAATCCTGATTAGGGTTGAGACTGTTGACGGCGGCGATTGGC-CGTCGCGGCG 179 379 239 439 9 200 AIGACGTICCGAAGTITACTCCAGGAGAIGCGGTCTAGGCCACACCGTGTAGTTCACGCC 1 ATGACGTTCCGAAGTTTACTCCAGGAAATGCGGTCTAGGCCACACGCGTGTAGTTCACGCC 260 GCCGCCTCAACCGCTAATAGTTCAGACCCTTTCAGCTGGTCGGAGCTCCCGGAGGTG http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers Gaps 9 Length 1535; 62; Indels /clone="GSITPGH44ZH11" /tissue_type="Hormone Treated Callus" /ecotype="Col-0" DB 4; /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" 88.1%; Score 1004.8; DB 4 94.1%; Pred. No. 1.2e-305; cive 0; Mismatches 62; BX824384.1 GI:42463622 HTC, GSLT CDNA. Arabidopsis thaliana (thale cress) Arabidopsis thaliana /plasmid="pCMVSPORT_6" /gene="At3g06380" Unpublished 2 (bases 1 to 1535) Query Match 88.1 Best Local Similarity 94.1 Matches 1078; Conservative Annotation Genoscope g

	Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons rosads; eurosida II; Brassicales; Brassicaceae; Arabidopais. 1 (bases 1 to 1036) 1 (bases 1 to 1036) 2 (astelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Femple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Phole Genome Sequence Comparisons and 'Phll-Length' cDNA Sequence Annotation 1 Unpublished (2104) 1 Contact: Genoscope 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE 2 mail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr The sequences are based on single pass reads. 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE 2 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr The sequence are based on single pass reads. 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE 2 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr The sequence are based on single pass reads. 3 rue Gaston Cremieux, CP 5706 - 91057 EVRY 3 ruy J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. WROY INRA: Clepet C., Caboche M. Mnotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). http://www.genoscope.cns.fr/externe/sequences/Banque_Projet EF/ES/ Anotation/Qualifiers 1 . 1036 Occation/Qualifiers Cacation/Qualifiers Colone="GSLTFB3382C05" Clone="GSLTFB3382C05" Clone="GSLTFB3382C05"							'Match 72.8%; Score 830.2; DB 5; Length 1036; Local Similarity 99.4%; Pred. No. 1.8e-250; Les 854; Conservative 0; Mismatches 3; Indels 2; Gaps 2;	1 ATGACGTICCGAAGTITACTCCAGGAAATGCGGTCTAGGCCACACCGTGTAGTICACGCC 60	61 GCCGCCTCAACCGCTAATAGTTCAGACCCTTTCAGCTGGTCGGAGCTCCCGGAGGGCTG 120	121 CTTAGAGAAATCCTGATTAGGGTTGAGACTGTTGACGGGGGGATTGGCCGTCGCGGGGA 180 	181 AACGTGGTGGCCGGCGTTTGTCGTAGCTGGAGGATTCTCACCAAGGAGTTGTA 240	241 GCTGTTCCTGAATTCTCCTCTAAATTGACTTTCCCTATCTCCCTCAAGCAGTCTGGTCCA 300	301 AGAGATTCTCTAGTTCAATGCTTTATAAAAGGTAATGGAAATACTCGATCGTATCTC 360 	361 TATCTCGGATTAACTACCTCTTTGACGGATAACGGGAAGTTTCTTCTTGCTGCTTCTAAG 420 [
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White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
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(bases 1 to 755)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Anll-Length' CDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Welssenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
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CTGAAGCGCCCAACTTGCACTGATTACATCTTTTTTTGCGTTCAGACGATATCTCAAAG
                                                                                                 TITGATGGTAGTCAGACCGGAGCGAAGATGCAGAAGAGCCGCTCTTCTAATTTCATC
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/mol_type="mRNA"
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Arabidopsis thaliana
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BX837992.1 GI:42532075
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Unpublished (2004)
Contact: Genoscope
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RESULT 6 BX837992

480

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Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
Litp://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                      Arabidopsis thaliana Full-length cDNA Complete sequence from clossITFB70ZH02 of Flowers and buds of strain col-0 of Arabidopsis
        541 CATGGATTATGGATATCCGATTTCTGCGTTTCAAGCGTTTGCTATCTGCCTGAGCAG 597
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Location/Qualifiers
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Pred. No. 7.1e-168;
0; Mismatches 268;
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/mol_type="mRNA"
/db_xref="taxon:3702"
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/plasmid="pCMVSPORT 6"
complement(1. .1281)
/gene="At5918680"
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A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="seed"
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/lab_host="B.coli"
/clome_lib="Arabidopsis developing seed"
/note="Grgar. Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"
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                                                                                                                                                                                                                                 Michigan State University DNA Sequencing Facility Arabidopsis Biological Resource Center, The Ohio State University, 309 Bot Zoology Bldgs, 1735 Nell Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.
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                                                                              Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI
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Pred. No. 1.8e-175;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                        organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
/clone="M39C9"
                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/ecotype="Columbia"
                                                                                                                                                                               Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
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Best Local Similarity 99.5%;
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Arabidopsis thaliana cDNA clone APZ42a03R 5', mRNA sequence.
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                                                                                                                                                                       GTTCAGACGATATCTCAAAGAGAAGCAACGCGTATCTTGGGAGAATGAGATCGAACTTCC
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 516)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and saize-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000) t ö 459 420 519 480 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/. Location/Qualifiers 159 120 219 GOCGATTGGCCGTCGCGGCGAAACGTGGTGGCTTGTGCGGCGTTTGTCGTAGCTGGAGG 180 279 240 339 300 399 360 09 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: KhoI" two 181 AFTCTCACCAAGGAGATTGTAGCTGTTCCTGAAFTCTCCTCTAAATTGACTTTCCCTATC 241 TCCCTCAAGCAGTCTGGTCCCAAGAGATTCTCTAGTTCAATGCTTTATAAAACGTAATCGA AATACTCAATCGTATCATCTCTCTCGGATTAACTACCTCTTTGACGGATAACGGGAAG TITCITCITGCTGCTTCTAAGCTGAAGCGCGCAACTTGCACTGATTACATCATCTTTG 361 TITCITCTTGTTGTTCTTAAAGTGAAGGGGGGAACTTGCACTGATTACATCTCTTTG TCCCTCAAGCAGTCTGGTCCAAGAGATTCTCTAGTTCAATGCTTTATAAAACGTAATCGA CGTTCAGACGATATCTCAAAGAGAAGCAACGCGTATCTTGGGAGAATGAGATCGAACTTC CCACACCGTGTAGTTCACGCCGCCGCCTCAACCGCTAATAGTTCAGACCCTTTCAGCTGG rcegaecrecegaegaecrecrracagaarecrearracegrragaerererreaege ATTCTCACCAAGGAGATTGTAGCTGTTCCTGAATTCTCCTCTAAATTGACTTTCCCTATC TCGGAGCTCCCGGAGGAGCTGCTTAGAGAAATCCTGATTAGGGTTGAGACTGTTGACGGC GGCGATTGGCCGTCGCGGAAACGTGGTGGCTTGTGCCGGCGTTTGTCGTAGCTGGAGG Gaps /tissue_type="aboveground organs"
/dev stage="two to six-week old"
/clone lib="Arabidopsis thaliana aboveground organs
six-week old" ö CCACACCGTGTAGTTCACGCCGCCGCTCAACCGCTAATAGTTCAGACCCT Length 516; Indels Research 45.3%; Score 516; DB 1; Le 100.0%; Pred. No. 3.4e-151; /organism="Arabidopsis thaliana" /mol_type="mRNA" /mol_type="columbia" /db_xref="texcn:3702" /clone="ApZ42a03R" 100.0%; Prec. ... The First Laboratory for Plant Gene Kazusa DNA Research Institute Arabidopsis thaliana (thale cress) Arabidopsis thaliana Contact: Brika Asamizu AV527654 AV527654.1 GI:8687182 516; Conservative 460 셤 ò

520 CTTGGAACAAATTCACGGTCTTTGATGGTAGTCAG 555

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AV527654 Arabidopsis thaliana aboveground organs two to six-week

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Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishiu,Y., Arakawa,T., Shibata,K., Shinagawa,A., Itoh,M., Hayashizaki,Y. and Shinozaki,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K., Iarge scale analysis of Arabidopsis full-length cDNA (Contact: Motcaki Seki Dlant Functional Genomics Research Group RIKEN Genomics Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Fal: 81-298-36-4359 Fax: 81-298-36-4359 Conditied Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
                                                                                                                                                                                                                                                                                       AU237181
AU237181 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-03-H24 5',
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/clone lib="RAFL16"
/note="Site_1: BamH1; Site_2: Sal1; dark-grown"
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39.4%; Score 449; DB 1; L
Best Local Similarity 99.3%; Pred. No. 5.7e-130;
Matches 449; Conservative 0; Mismatches 3;
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/mol_type="mRNA"
/db_xref="taxon:3702"
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Arabidopsis thaliana
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AU237181
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| organism="Marabidopsis thaliana" |
| organism="Marabidopsis thaliana" |
| multiple="mnNA" |
| do_tryp="Columbia" |
| db_xref="taxon:3702" |
| db_xref="taxon:3702" |
| db_xref="Plant 3 weeks old, three days post infection" |
| db_ref="plant 3 weeks old, three days post infection" |
| clone lib="Infected Arabidopsis Leaf" |
| note="Organ: Leaf; Vector: pBluescript; Mixed cDNA |
| ibrary of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT selected."
                                                                                                                                                          BU636137
046A07 Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosida II, Brassicales, Brassicaceae, Arabidopsis.
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8ST sequencing of Erysiphe cichoracearum infected Arabidopsis
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Tel: +45 96358467
Fax: +45 98141808
Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plants
Unpublished (2002)
Contact: Karen G. Welinder
Institut for bioteknologi
Aalborg Universitet
                                                                                                                                                                                                                                BUĞ36137
BUG36137.1 GI:23303392
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                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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                                                                                                                                                                                                             sequence.
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/mol type="mRNA"

/mol type="Columbia"

/ecocype="Columbia"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F13831 420 bp mRNA linear EST 06-APR-1995 ATTS4753 Versailles-VB Arabidopsis thaliana cDNA clone VBVOC09 5' similar to phosphodiesterase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   607 ACATATGAGCTGAATGTCTTAGGATCCCGGGGACCAAGAAGATGCAATGTCTTATGGAC 666
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
127 CGCAGCGTGGTGGCTTTGTCGTCGTGGCTGGCTGCTACTTATGAACGAAACC 186
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Contact: Desprez T., Amselem J., Chiapello H., Rouze P., Caboche M., Hofte H.
                                                                                                                                                247 CCAAGGGATTCACTGGTTCAATGCTTTATCAAACGTAATCGAATTACGCAATCATACAT
                                                                                                                                                                                                                                                                                    AAGCTGAAGCGCGCAACTTGCACTTACATCATCTCTTTGCGTTCAGACGATATCTCA
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                                         GTAGCTGTTCCTGAATTCTCCTCTAAATTGACTTTCCCTATCTCCCTCAAGCAGTCTGGT
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Laboratoire de Biologie Cellulaire
Route de Saint-Cyr,78026 Versailles Cedex,France
Email: thierry@versailles.inra.fr.
Location/Qualifiers
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/deV stage="taxon:3702"
/deV stage="taxon:3702"
/clone_lib="Infected Arabidopsis Leaf"
/clone_lib="Infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
/ibrary of Arabidopsis and E. cichoracearum infected leaf
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
selected."
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EST sequencing of Erysiphe cichoracearum infected Arabidopsis
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                                                387 GCTGTTCCTGAATTCTCCTCTAAATTGACTTTCCCTATCTCCCTCAAGCAGTCTGGTCCA
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Sohngaardsholmavej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
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/mol_type="mRNA"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                        CTGAAGCGCGCAACTTGCACTGATTACATCAT 452
                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Location/Qualifiers
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Institut for bioteknologi
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BU635249.1 GI:23302504
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Matches 534; Conservative
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7585 Lambda-PRL2 Arabidopsis thaliana CDNA clone 124E22T7, mRNA
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 358)
Newman,T., deBruila,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,R. and Somerville,C.
Genes galore: a summary of methods for accessing results from
                                                                                                                                                                          -------GCCGCCTCAACCGCTAATAGTTCAGACCCTTTCAGCTGGTCG 102
                                                                                                                                                                                                                                                                          137 CTTGCCGCCGCCGCAGCTGCCGATTCCACTTCTGTGTCATCGCAAGATTATCGCTGGTCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 TCTCAAGCAGCCTGGTCCAAGGGATTCACTGGTTCAATGCTTTATCAAACGTAATCGAAT 436
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                                                                                                      28;
                                                              DB 5; Length 728
                                                          Score 333; DB 5; Length 72
Pred. No. 3e-93;
0; Mismatches 135; Indels
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                                                            Match 29.2%;
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/note="Organ: Leaf, Vector: pBluescript; Mixed cDNA
library of Arabidopsis and E. cichoraccarum infected leaf
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
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Arabidopsis thaliana
Bukaryota, Virigiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Wagnoliophyta, eudicotyledons; core eudicotyledons; rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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EST sequencing of Erysiphe cichoracearum infected Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                           181 GATTACATCATCTCTTTGCGTTCAGACGATATCTCAAAGAGAAGCAACGGTATTCTTGGG
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                                                                                                                                                                                                                                                                                                  TTGACGGATAACGGGAAGTTTCTTCTTGCTGCTTCTAAGCTGAAGCGCGCAACTTGCACT
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                                                                                                                                                                                                             TTTATAAAAACGTAATCGAAATACTCAATCGTATCATCTTTATCTCGGGATTAACTACCTCT
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Schngaardeholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
                                        Query Match
34.0%; Score 388; DB 8; I
Best Local Similarity 98.3%; Pred. No. 9.8e-111;
Matches 413; Conservative 0; Mismatches 5;
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Location/Qualifiers
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Unpublished (2002)
Contact: Karen G. Welinder
Institut for bioteknologi
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/note="wetcor: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Inmbda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed CDNA.
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On Jan 7, 1998 this sequence version replaced gi:948641.
Contact: Thomas Newman
MSU-DOB Plant Research Laboratory
Michigan State University
Michigan State University
Lansing, Mi
Tel: 517-35-0854
Fax: 517-35-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7.
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/ecctype="Columbia"
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/ Cgn2 6/ptcdata/1/ina/5_COMB.seq:*
/ Cgn2 6/ptcdata/1/ina/6_COMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-670-592-6

US-08-714-991-6

US-09-032-365A-7

US-08-697-766A-11

US-09-032-365A-61

US-09-032-365A-69

US-08-922-267A-7

US-08-922-267A-7

US-08-922-267A-7

US-08-936-707A-7

US-08-936-707A-7

US-09-248-203-7

US-09-248-203-7

US-09-365-918C-9

US-09-406-071-7

US-09-406-071-7

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US-09-406-071-7

US-09-91-365A-64

US-09-032-365A-64

US-09-032-365A-64

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6.3%; Score 72; DB 3; Length 299;
Best Local Similarity 72.1%; Pred. No. 1.3e-13;
Matches 93; Conservative 0; Mismatches 36; Indels
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Patent No. 6476212

FGENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lic, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DER.
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT APPLICATION NUMBER: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program

SEG ID NO 6623

SEG ID NOS: 7600

SEG ID NOS: 7600
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    NAME/KEY: misc_feature
    OTHER INCORMATION: Incyte ID No. 6476212 700352120H1
    NAME/KEY: unsure
    LOCATION: 102, 134, 269
    CTHER INCORMATION: a, t, c, g, or other
    US-09-313-294A-6623
                                               US-08-630-592-3

US-08-714-991-3

US-08-714-991-3

US-08-90-32-365A-9

US-08-95-918C-8

US-08-697-766A-8

US-08-697-766A-6

US-08-697-766A-6

US-08-631-200-1

US-08-631-200-1

US-08-95-53-1

US-08-95-53-1

US-08-93-707A-1

US-08-96-706A-1

US-08-96-706A-1

US-08-96-706A-1

US-08-96-706A-1

US-09-14-98C-1

US-09-140-98C-1

US-09-140-98C-1

US-09-102-365A-18
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                                                     GCCTGTGAA 1140
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ORGANISM: Zea mays
 \begin{array}{c} \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf{v} \cdot \mathbf
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APPLICANT: NAGGERT, Juergen
TITLE OF INVENTION: OBESITY ASSOCIATED GENES
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERIFICS:
LENGTH: 1426 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97; Indels
                                                                                                                                                                         ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 3400 Embarcadero Center, Suite 3400 CTXY: San Prancisco STATE: Galifornia
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PCDOS/MSDOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%; Score 66.8; DB 2; Best Local Similarity 57.1%; Pred. No. 1.9e-11; Matches 153; Conservative 0; Mismatches 97;
                    APPLICANT: Nishina, Patsy
APPLICANT: No. 5770432enTrauth, Konrad
APPLICANT: Naggert, Juergen
APPLICANT: No. 5770432th, Michael
TITLE OF INVENTION: Obesity Associated Genes
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGRAT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REEERRENCE/DOCKET NUMBER: 36,677
RELECOMMUNICATION INFORMATION:
TELEFAX: (415) 7811989
TELEFAX: (415) 7811989
TELEFAX: (415) 398349
TELEFX: 910 277299
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1426 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Patent No. 5776762
GENERAL INFORMATION:
APPLICANT: NORTH, Michael
APPLICANT: NSHINA, Patey
APPLICANT: No. 5776762en-Trauth, Konrad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-630-592-6
                                                                                                                                                                                                                                                                                        ZIP: 941114187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                  COUNTRY:
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US-08-714-991-6
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992 GTGAAGCAGGCAGACATCTGAGATCATACTCCAGTTTGGGAAAGTTGGGAAGGACA 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.9%; Score 66.8; DB 2; Length 1426; Best Local Similarity 57.1%; Pred. No. 1.9e-11; Matches 153; Conservative 0; Mismatches 97; Indels 18
TITLE OF INVENTION: OBESITY ASSOCIATED GENES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: PLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/714,991

FILING DATE:

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:

NAME: SHERWOOD, Pamela J.

REGISTRATION NUMBER: 36,677

REGISTRATION NUMBER: 36,677

REJERPAN: 415-494-8701

TELERPAN: 415-494-8701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1112 GCAGTTTTGAAACCAGAATTGCCTGTGA 1139
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,918C
                                                                                                                                                                                                                                   FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/GOCKET NUMBER: MNI-007CPDV2CPA
TELECOMMUNICATION INFORMATION:
TELEPAK: (617)227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LEMETH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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US-08-955-918C-11
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Patent No. 6268130
GENERAL INFORMATION:
APPLICANT: ALLOYN, Patrick, and Moore, Karen
TITLE OF INVENTION: RP Compositions and Therapeutic and
TITLE OF INVENTION: Diagnostic Uses Therefor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                            COMPUTER: IBM COMPACTULE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 536
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                    ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/POCKET NUMBER: SEQ-2CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1426 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                Diskette
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
CORRESPONDENCE ADDRESS:
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                                                                                   STATE: CA
COUNTRY: US
ZIP: 94301
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US-08-955-918C-11
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                                                   18; Gaps
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; Batent No. 6114502
; GENERAL INFORMATION:
; APPLICANT: No. 6114502th, Michael
APPLICANT: No. 6114502th, Michael
APPLICANT: No. 6114502th, Trauth, Konrad
; TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
; TITLE OF INVENTION: NEUROSENSORY DEFECTS
NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

5.9%; Score 66.8; DB 3;

Best Local Similarity 57.1%; Pred. No. 2.2e-11;

Matches 153; Conservative 0; Mismatches 97;
                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1112 GCAGTTTTGAAACCAGAATTGCCTGTGA 1139
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TELEPHONE: 650-327-3400
TELEFAX: 650 327-3231
                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,0
REFERENCE/DOCKET NUMBER:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1890 base pairs
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STRANDEDNESS: double
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COUNTRY: U
ZIP: 94301
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2e-11;
thes 97; Indels 18
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLM PC compatible
COMPUTER: Ploppy disk
COMPUTER: BLM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,766A
FILING DATE: 29-AUG-1996
PRIOR APPLICATION NUMBER: US/08/697,766A
FILING DATE: 39-AUG-1996
PRIOR APPLICATION NUMBER: 39,030
REFERENCE/POCKET NUMBER: 39,030
REFERENCE/POCKET NUMBER: 39,030
REFERENCE/COMPUTICATION INFORMATION:
TELEPRATION NUMBER: 39,030
TELEPRATION SILVERY 100
TELEPRATION NUMBER: 11:
TELEPRATION SILVERY 100: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDBURSS: single
TOTAL SILVERY 100
THE COMPUTER SILVERY 100
TELEPRATION SILVERY 100
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US-09-032-365A-61
; Sequence 61, Application US/09032365A
; Patent No. 6114502
; GENERAL INFORMATION:
; APPLICANT: No. 6114502th, Michael
; APPLICANT: No. 6114502th, Michael
; APPLICANT: No. 6114502en-Trauth, Konrad
; TITLE OF INVENTION: GENE FAMILY ASSOCIATED
; TITLE OF INVENTION: NEUROSENSORY DEFECTS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
5.9%; Score 66.8; DE
Best Local Similarity 57.1%; Pred. No. 2e-11
Matches 153; Conservative 0; Mismatches
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285 Hamilton Avenue, Suite 200
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STREET: 285
CITY: Palo
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US-08-697-766A-11
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Sequence 7, Application US/08829553

Patent No. 5817762

GENERAL INFORMATION:
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSES: Pennie & Edmonds
CORRESPONDENCE PRODUCE OF PARTY AND CORRESPONDENCE ADDRESSES:
ADDRESSES: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1420 TCGAGCTGCAAAACAAGACACCTGTCTGGAATGATGACACACAGTCCTATGTACTCAACT 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.9%; Score 66.8; DB 2; Length 2040; Best Local Similarity 57.1%; Pred. No. 2.3e-11; Matches 153; Conservative 0; Mismatches 97; Indels 18
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/631,200
FILING DATE: 12-APR-1996
FILING DATE: 12-APR-1996
FILING DATE: 12-APR-1996
FILING COLUZZI, LAURA A.
NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 7853-057
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2040 base paix
TYPE: nucleic acid
STRANDEDNESS: unknown
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) LOCATION: 153..1670

US-08-631-200-7
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COMPUTER READABLE
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Patent No. 5646040
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KleyT, Patrick W.
APPLICANT: MOOTE, KATEN J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1376 TCCATGGGGGGTCACACACAGGGCTCCGTGAAGAACTTCCAGGATCATCCATGGCAATGACC 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1316 TCGAĞCTGCAAAACAAGGACCTGTCTGGAATGATGACACACAGTCCTATGTACTCAACT 1375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 66.8; DB 3; Length 1936;
57.1%; Pred. No. 2.3e-11;
tive 0; Mismatches 97; Indels 18;
                                                   COMPUTER: USA
ZIP: 94301
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSRO for Windows Version 2.0
SOFTWARE: FastSRO for Windows Version 2.0
SOFTWARE: Value Number: US/09/032,365A
FILING DATE:
FILING DATE:
PLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
FILING DATE:
APPLICATION NUMBER: SS6
FILING DATE:
APPLICATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 36,677
TELECOMMUNICATION:
TELEPHONE: 650-327-3400
TELERAN: 650-327-340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1112 GCAGTTTTGAAACCAGAATTGCCTGTGA 1139
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SEQUENCE CHARACTERISTICS:
LENGTH: 1936 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.19
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: CDNP
US-09-032-365A-59
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STATE: New York
COUNTRY: U.S.A.
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US-08-631-200-7
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,553
FILING DATE: 28-MAR-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION S30
FILING DATE: 12-APR-196
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-085
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) / Journal TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
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Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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APPLICANT: Kleyn, Patrick W.
APPLICANT: MOOF, Karen J.
TILE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1420 redaderecaaaacaadeacacerereradaardardacaeacacacerecrareracreaacr 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          872 TGGTGCTGAGCAACAACAAGCTCCACGGTGGCATGAGCAGTTACGTTGCTGGTGCTTAAATT 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.9%; Score 66.8; DB 2; Length 2040; Best Local Similarity 57.1%; Pred. No. 2.3e-11; Matches 153; Conservative 0; Mismatches 97; Indels 18
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,553
FILING DATE: 28-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1642 ccascriccacaccascrecerscea 1669
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                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08922267A
Patent No. 5861239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153..1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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US-08-829-553-7
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US-08-936-707A-7

Sequence 7, Application US/08936707A

Sequence 7, Application US/08936707A

GENERAL INFORMATION:

APPLICANT: Kleyn, Partick W.

APPLICANT: Moore, Karen J.

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1420 TCGAGCTGCAAAACAAGACACCACTGTCTGGAATGATGATGACACACAGAGTCCTATGTACTCAACT 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  872 TGGTGCTGAGCAACAAAGCTCCACGGTGGCATGAGCAGTTACGTTGCTGGTGCTTAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           932 TCCATGGTCGAGTCACAGTGGCTTCGGTTAAGAACTTTCAGCTTGTGGCCAGTTAGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 66.8; DB 2; Length 2040; 57.1%; Pred. No. 2.3e-11; Live 0; Mismatches 97; Indels 18
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/922,267A
FILING DATE: 2-SEP-1997
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Karen J.
1: COMPOSITIONS FOR THE TREATMENT AND
1: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
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Best Local Similarity 57.1%; Pred. No. 2.3e-11;
Matches 153; Conservative 0; Mismatches 97; Indels 18.
                   CILII New York
COUNTRY: U.S.A.

ZATAE: New York
COUNTRY: U.S.A.

ZHE: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,706A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CCTUZZI, LBULTA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERRING/POCKET UNBER: 30,742
REJECTOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 869-9741/8864
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Fatent No. 6043346
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
TITLE OF INVENTION: COMPOSITIONS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF BODY WE:
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 869-9741/88
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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STATE: New York
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-936-706A-7
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Sequence 7. Application US/08936706A
Patent No. 5876919
GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1420 rcaagcracaaaacaacaccrcrcrcraaardarcacacacacrccrargracrcrakacr 1479
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                                                                   CITI:

STATE: New You.

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: Plopy disk

COMPUTER: PREPRIED FORMS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/936,707A

FILING DATE: 24-SEP-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: COLUZI, LAURA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-100

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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1155 Avenue of the Americas
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
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153..1670
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MOLECULE TYPE: DNA
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US-08-936-707A-7
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Sequence 7. Application US/09406071
Patent No. 6207386
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds Lip
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1420 regaderigeaaaacaacacerereregaarigargacacacacrerrargracreraacr 1479
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                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/248,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1112 GCAGTTTTGAAACCAGAATTGCCTGTGA 1139
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                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 24-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-100
TELECHONE: (212) 790-9090
TELERENCE: (212) 669-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                TELBETK: (212) BOJ TELBETK: (512) BOJ TELBETK: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
ILENGTH: 2040 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGLE
STRANDEDNESS: SINGLE
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
153..1670
                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-09-248-203-7
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US-09-406-071-7
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1480 TCCATGGGCGCGTCACACAGGCCTCCGTGAAGAACTTCCAGATCATCCATGGCAATGACC 1539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66.8; DB 3; Length 2040;
Pred. No. 2.3e-11;
0; Mismatches 97; Indels 18
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,071
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TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: 08/936,707
                                                                                                                                                                                                                                                                                                                               NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78 TELECOMMUNICATION INFORMATION:
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Best Local Similarity 57.1%;
Matches 153; Conservative
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ATTORNEY/AGENT INFORMATION:
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Sequence 31303, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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4.6%; Score 53; DB 6; Length 924;
Best Local Similarity 62.4%; Pred. No. 1.2e-07;
Matches 83; Conservative 0; Mismatches 50; Indels
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US-10-750-185-63480

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US-10-955-561-13327

US-10-137-465-13

US-10-750-185-53467

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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
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; ORGANISM: Bovine 19866881111971
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LENGTH: 924
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Query Match
Best Local Similarity
Matches 72; Conserva
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                                                                     APPLICANT: Kolpproder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
TITLE OF INVENTION: Muddler (metY)
FILE REFERENCE: 1311-0006-US
CURRENT APPLICATION NUMBER: US/10/525,710
CURRENT FILING DATE: 2003-08-26
PRIOR PILING DATE: 2003-08-26
PRIOR PILING DATE: 2003-08-26
PRIOR FILING DATE: 2003-08-26
PRIOR FILING DATE: 2003-08-26
NUMBER: OF SCO IN NOS: 79
SEQ ID NOS: 79
SEQ ID NOS: 79
SEQ ID NO 7
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US-11-121-086-94/C
US-11-121-086-94/C
US-11-121-086-94 Application US/11121086
; publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NUELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; TITLE REFERENCE: 09138.6000-000000
; FILE REFERENCE: 09138.6000-000000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
: LENGTH: 100387
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Pred. No. 2.3;
0; Mismatches 99; Indels 0;
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3.2%; Score 36; DB 6; Length 1293;
Best Local Similarity 54.5%; Pred. No. 0.1;
Matches 72; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
3.1%;
Best Local Similarity 49.0%;
Matches 95; Conservative
Publication No. US20050260721A1
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                                         Kroger, Burkhard
Zelder, Oskar
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US-11-121-086-94
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; LOCATION: (1)..(1293)
US-10-525-710-7
                   GENERAL INFORMATION:
APPLICANT: Kroger, Br
APPLICANT: Zelder, CAPPLICANT: Schroder, Schroder,
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82657 Greirecresreirrireachaensecenceaaracheentearandricantrichan 82598
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971 AGCTTGTGGCAGTTAGTGACTGTGAAGCAGGGCAGACATCTGAGAGGATCATACTCCAGT 1030
                                                                                                                                  1031 TIGGGAAAGTIGGGAAGGACAIGTITACCAIGGATTAIGGATAICCGAITTICIGCGITTC 1090
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| Publication No. US2000266603A1
| GENERAL INFORMATION:
| APPLICANT: MMI GENOMICS, INC.
| APPLICANT: ROSENFELD, David
| APPLICANT: ROSENFELD, David
| APPLICANT: ROSENFELD, David
| APPLICANT: ROSENFELD, David
| APPLICANT: PARTIN, Dennis
| APPLICANT: PARTIN, Dennis
| APPLICANT: PARTIN, Dennis
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| FILE REFERENCE: MMILLO0-2
| CURRENT APPLICATION NUMBER: US/10/750,185
| CURRENT PILING DATE: 2003-12-31
| PRIOR APPLICATION NUMBER: US 60/437,482
| RINGRAD APPLICATION NUMBER: US 60/437,482
| NUMBER OF SEQ ID NOS: 64922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 179, Application US/10667295
; Sequence 179, Application US/2050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURENT APPLICATION NUMBER: US/10/667, 295
; CURENT FILING DATE: 2003-09-17
; RUMBER OF SEQ ID NOS: 263
; NUMBER OF SEQ ID NOS: 263
; SEQ ID NO 179
; ELEVINE NO 179
; LENGTHARE: PASESEQ for Windows Version 4.0
; SEQ ID NO 179
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; NAME/KEY: misc feature
; LOCATION: (1)...(1161)
; OTTER INFORMATION: Ceres Seq. ID no. 12598265
US-10-667-295-179
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APPLICANT: GORDON, STEPHEN
APPLICANT: GORDON, STEPHEN
APPLICANT: GORDON, STEPHEN
APPLICANT: GORDON, STEPHEN
APPLICANT: BILLAULT, ALAIN
TITLE OF INVENTION: PROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: PROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: DNA LIBRARY. APPLICATION OF
TITLE REFERENCE: 05394.0011-00000
CURRENT APPLICATION NUMBER: US/10/802,796
CURRENT FILING DATE: 12094-03-18
PRIOR PILING DATE: 12999-04-16
PRIOR PILING DATE: 1999-04-16
PRIOR PILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
SHOW RELING DATE: 1999-04-16
SHOW BELOW OF SEQ ID NOS: 743
SOFTWARE: PALCHIN VEY: 2.2
SEQ ID NO 127
LENGTH: 315
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Pred. No. 0.27;
0; Mismatches
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENONICS, INC.
APPLICANT: MRISE, Sue K.
APPLICANT: KERK, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
                           OLE, STEWART BUCHRIESER-BROSCH, ROLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
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2.9%;
Best Local Similarity 62.2%;
Matches 51; Conservative (
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US-10-802-796-127
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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LOCATION: (153)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13264
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER: OF SEG ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13264
LENGTH: 110711
                                                                                                                                                                                                                                                             201 CGTTTGTCGTAGCTGGAGGATTCTCAAGGAGATTGTAGCTGTTCCTGAATTCTCCTC 260
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                                                                                                                                                                                                                                                                                                                                                           261 TAAATTGACTTTCCCTATCTCCCTCAAGCAGTCTGGTCCAAGAGATTCTCTAGTTCAATG 320
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                                                                                                                                                             Query Match
3.0%; Score 33.8; DB 6; Length 1389;
Best Local Similarity 48.7%; Pred. No. 0.6;
Matches 92; Conservative 0; Mismatches 97; Indels 0
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Best Local Similarity 54.4%; Pred. No. 10;
Matches 68; Conservative 0; Mismatches
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Publication No. US20050250104A1
                                                                    ; TYPE: DNA
; ORGANISM: Bovine 19866880552958
US-10-750-185-64773
SOFTWARE: PatentIN version 3.1
SEQ ID NO 64773
LENGTH: 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 TTTGACGGA 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                               240 AGCTGTTCCTGAATTCTCCTCTAAATTGACTTTCCCTATCTCCCTCAAGCAGTCTGGTCC 299
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APPLICANT: PMI GENOWICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: DENISE, Sue K.
APPLICANT: RERR, Atchard
APPLICANT: RESERVED, David
APPLICANT: ROSENFELD, David
APPLICANT: RATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILIOO-2
CURRENT APPLICATION NUMBER: US, 10, 750, 185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION WHERE: US, 60/437, 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.6; DB 6; Length 867;
Pred. No. 1.1;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                 Query Match 2.9%; Score 33; DB 6; Length 2848; Best Local Similarity 51.7%; Pred. No. 1.8; Matches 75; Conservative 0; Mismatches 70; Indels
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MMILIO0-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2000-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 CIATCICGGATTAACTACCICTTIGAC 386
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US-10-750-185-26853/c
; Sequence 26853, Application US/10750185
; Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Bovine 19866880569853
US-10-750-185-26853
                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Bovine 19866881140451
US-10-750-185-56373
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 26853
LENGTH: 867
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Best Local Similarity 60.99
Marches 53; Conservative
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LENGTH: 2848
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RESULT 10

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1449 TITTAGTTATICCTGCTGTTTTTTTTTAATITCTTATGAGTTACTCCAGCTACTAGTTTT 1508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 GICCAAGAGAITCICITAGITCAAIGCITITAIAAAACGIAAICGAAAIACICAAICGIAIC 355
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Sequence 41445, Application US/10750185

publication No. US20050260603A1

GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MMI GENOMICS, INC.
APPLICANT: RERR Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: PANTIN, Dennis
TILLE OF INVENTIN, Dennis
FILE REFERENCE: MAILIOG-2
CURRENT FALING DATE: 2003-12-31
FRICK APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 41445
LINGTH: 2195
LINGTH: 2195
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIJON-2
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 55303
LENGTH: 1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 ATCTCTATCTCGGATTAACTACCTCTTTGACGGATAACGG 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 55303, Application US/10750185
Publication No. US20050260603A1
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; ORGANISM: Bovine 19866880795732
US-10-750-185-55303
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; ORGANISM: Bovine 19866880956289
US-10-750-185-41445
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
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NUMBER OF SEQ ID NOS: 64922
SOFWARE: Patentin version 3.1
SEQ ID NO 2925
LENGTH: 600
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US-10-750-185-25701/c
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  369 ATTAACTACCTCTTTGACGGATAACGGGAAGTTTCTTCTTGCTGCTTCTAAGCTGAAGCG 428
                                                                                                            790 TITITACAAAACTITIGGIGIAGCATAATAAAATTATICTGACAGCTICAATGCCAAAATG 731
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APPLICANT: WHI GENOMICS, INC.
APPLICANT: PAPLICANT: CENTS.
APPLICANT: CENTS.
APPLICANT: RERR, RICLAXA
APPLICANT: RERR, RICLAXA
APPLICANT: ROSENFELD, David
APPLICANT: APPLICANT: Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIL100-23
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PELLON NUMBER: US 60/437,482
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 57408
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Sequence 2925, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: RERE, Richard

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR PLING DATE: 2002-12-31
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Publication No. US20050260603A1
                                                                                                                                                              429 CGCAACTTGCACTGATTAC 447
                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Bovine 19866881175911
US-10-750-185-57408
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US-10-750-185-57408/c
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                                                                                                                                                                                                                                                                                                                                                                                   133 AAACCCATGTCAATCACACATTTGGAAGCAGAGRCAGGTGATACCCCATCACAAGTACA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 ATAMARCGIAATCGAAATACTCAATCGIATCTCTCTTTCTCCGGATTAACTACCTCTTT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 TTCAGCCTGAAGCAGCTTTCACAATACTTTTATATTTTTTCTTGAATTATTTAGAGCCTT 215
                                                                                                                                                                                                                             205 TGTCGTAGCTGGAGGATTCTCACCAAGGAGATTGTAGCTGTTCCTGAATTCTCCTCTAAA
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                                                                                                                                                                          0; Gaps
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                                                                                                        Score 31.4; DB 6; Length 600; Pred. No. 2.3; 1; Mismatches 92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57709, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MAI GENONICS, INC.
APPLICANT: FOR KERR, Richard
APPLICANT: ROSENEELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN Demnis
APPLICANT: FANTIN Demnis
APPLICANT: CONPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 GAAGCGCCAACTTGCACTGATTACATCA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: MAILIOG-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SOFTWARE: Patent 1793
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Bovine 19866880388936
US-10-750-185-57709
                                                                                                                 Query Match
Best Local Similarity 48.0%;
Matches 86; Conservative
; TYPE: DNA
; ORGANISM: Bovine MMBT17358
US-10-750-185-2925
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Search completed: December 26, 2005, 07:23:33 Job time : 657 secs

Scoring table:

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                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plant, salt tolerance; crop improvement; cold tolerance; oxidative stress; drought resistance; TUBBY-like protein; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana TUBBY-like protein (TLP) 9 encoding cDNA.
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product= "Arabidopsis thaliana TLP9 protein"
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                             The invention relates to Arabidopsis TUBBY-like proteins (TLP) and their corresponding nucleic acid sequences. The invention also relates to a transformed cell or a transgenic plant containing TLP nucleic acid and a transformed cell or a transgenic plant lacking TLP nucleic acid and a transformed cells or a transgenic plant lacking TLP nucleic acid. The TLP polypeptides and nucleic acids are useful for producing transgenic or transformed cells or plants having higher tolerance to salt, chilling, pathogens, oxidative stress or water-deficit. The present sequence is the Arabidopsis thaliana TLP9 encoding cDNA. The Arabidopsis thaliana TLP9
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1080 1080 1140 1020 This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up-or down-regulated in transgenic plants overexpressing the heterodimeric E2Fs/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, blochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or 960 900 960 781 TCATCACCAGTCTTTAGGTCTCACTCAAAACCATTGCGCAGTAATAGTGCATCATGTAGC 840 GACTCAGGCAACAACATGGGAGATCCACCATTGGTGCTGAGCAACAAAGCTCCACGGTGG CATGAGCAGTTACGTTGCTGGTGCTTAAATTTCCATGGTCGAGTCACAGTGGCTTCGGTT GTGGCAGTTAGTGACTGTGAAGCAGGCCAGACATCTGAGAGGATC ATACTCCAGTTTGGGAAAGTTGGGAAGGACATGTTTACCATGGATTATGGATATCCGATT TCTGCGTTTCAAGCGTTTGCTATCTGCCTGAGCAGTTTTGAAACCAGAATTGCCTGTGAA ATACTCCAGTTTGGGAAAGTTGGGAAGGACATGTTTACCATGGATTATGGATATCCGATT GACTCAGGCAACAACCTGGGAGATCCACCATTGGTGCTGAGCAACAAAGCTCCACGGTGG CATGAGCAGTTACGTTGCTGCTTAAATTTCCATGGTCGAGTCACAGTGGCTTCGGTT plants SegID 943. metabolism growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon Thale cress cDNA upregulated in E2Fa/Dpa expressing transgenic; E2Fa/DPa transcription Claim 1; SEQ ID NO 943; 134pp; English ĸ BP. Vlieghe ADN73048 standard; cDNA; 1143 20-OCT-2003; 2003WO-EP011658. 18-OCT-2002; 2002EP-00079408 (first entry) De Veylder L, (CROP-) CROPDESIGN NV Arabidopsis thaliana

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Riechmann JL, Haake V, Dubell
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sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/ or carbon metabolism or they function as transcription factors. This polymuclaotide sequence is thale cress cDNA upregulated 1.3 fold or more in plants overexpressing the EZFs/DPa transcription factor, given in an exemplification of the invention.
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                                                                                                                                                           0; Indels
                                                                                                                                 Query Match 100.0%; Score 1140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1140; Conservative 0; Mismatches
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                                             960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; transcription factor; transgenic plant; abiotic stress tolerance; semotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1081 TCTGGGTTTCAAGCGTTTGCTATCTGCCTGAGCAGTTTTGAAACCAGAATTGCCTGTGAA
1081 TCTGCGTTTCAAGCGTTTGCTATCTGCCTGAGCAGTTTTGAAACCAGAATTGCCTGTGAA
901 CATGAGCAGTTACGTTGCTGGTGCTTAAATTTCCATGGTCGAGTCACATGGTCGAGTTCGGTT
                                                                                                                               961 AAGAACTTTCAGCTTGTGGCAGTTAGTGACTGTGAAGCAGGGCAGACATCTGAGAGGATC
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Sherman BK;
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Keddie JS,
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23-MAR-1999;
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increased sensitivity to ACC, altered sugar sensing, increased tolerance
to sugars, altered carbon/nitrogen sensing, early flowering, late
flowering, altered flower structure, loss of flower determinacy, reduced
fertility, altered shoot meristem development, altered branching pattern,
altered stem morphology, altered vascular tissue structure, reduced
aptical dominance, altered trichome density, altered trichome development,
altered trichome structure, altered trichome development,
altered trichome structure, altered seed ripening, altered seed
avoidance, altered seed development, altered phase change,
caltered cell proliferation, altered coll differentiation,
cc altered senescence, abnormal embryo development, altered phase change,
altered senescence, abnormal embryo development, altered phase change,
caltered senescence, abnormal embryo development, altered phase change,
caltered senescence, abnormal embryo development, altered plasse change,
collant size, increased biomass, large seedlings, dwarfed plants, dark
cgreen leaves, change in leaf shape, increased leaf size and mass, light
cgreen leaves, change in leaf shape, increased leaf size and mass, light
cgreen leaves, change in leaf shape, altered abed seed shape, large
seed, increased leaf wax, increased leaf fatty acids, altered seed oil
content, altered seed protein content, altered seed shape, large
content, altered seed protein content, altered seedsprenyl content,
altered leaf prenyl lipid content, increased anthocyanin levels, and
content part of the printed specification, but was obtained in
core form part of the printed specification, but was obtained in
celetronic format directly from WIPO at
cft._sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 267; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Score 572.8; DB 12
Pred. No. 1.6e-177;
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tches 852; Conservative
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                                                                                   CGTTGCATCATGGATACAATACCTATGAGCATCGTGGAGTCGCGAGGAGTAGTAGCTTCA
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            CGTTGCATCGATACAATACCTATGAGCATCGTGGAGTCGCGAGGAGTAGTAGCTTCA
                           TTGCGCAGTAATAGTGCATCATGTAGCGACTCAGGCAACAACCTGGGAGATCCACCATTG
                                                                                                                                               -------GCTCAAGCCACCTGAAAGAACACATTA
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                                                                GTGCTGAGCAACAAAGCTCCACGGTGGCATGAGCAGTTACGTTGCTGGTGCTTAAATTTC
                                                                                                                                                                                                                                                                                       AGTGACTGTGAAGCAGGCAGACATCTGAGA------GGATCATACTCCAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana TUBBY-like protein (TLP) 11 encoding cDNA
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1. .1140
14. stags a /product = "Arabidopsis thaliana TLP11 protein"
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P-PSDB; ADW64865.
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99US-0160741P.
99US-0160767P.
99US-0160767P.
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988 GGAATGTCACCGGAGAGGCGAGGCGAGTTATATTTCCAGTTTGGGAAAGTCGGGAAA 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic plant; plant; genetically modified cell; environmental stress; ribozyme creation; disease resistance; stress tolerance;
                GCATCATGTAGCGACTCAGGCAACAACCTGGGAGATCCACCATTGGTGCTGAGCAACAAA
                             GCTCCACGGGGGATGAGGTTACGTTGCTGGTGCTTAAATTTCCATGGTCGAGTCACA
                                                                                         868 ACACCACGGTGGCACGAGCTACGCTGCTGGTGCTTGAATTTCCATGGCCGTGTCACA
                                                                                                                             GTGGCTTCGGTTAAGAACTTTCAGCTTGTGGCAG-----TTAGTGACTGTGAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana expressed sequence related polynucleotide #879
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Page A, Mathew AV, Ledford BL, Woessner
Kricker M, Slater T, Davis KR, Allen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fungicide screening; insecticide screening; gene; ds
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PRICE J L.
RAINES T M.
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HAAS W D.
GARCIA C A.
KRICKER M.
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LEDFORD B L.
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DAVIS K R.
ALLEN K.
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Rameaka JG,
Garcia CA, 1
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                                                                               The invention relates to Arabidopsis TUBBY-like proteins (TLP) and their corresponding nucleic acid sequences. The invention also relates to a transfermed cell or a transgenic plant containing TLP nucleic acid and a transformed cell or a transgenic plant lacking TLP nucleic acid and a polypeptides and nucleic acids are useful for producing transgenic or transformed cells or plants having higher tolerance to salt, chilling, pathogens, oxidative stress or water-deflicit. The present sequence is the Arabidopsis thaliana TLP11 encoding cDNA. The Arabidopsis thaliana TLP11 encoding cDNA. The Arabidopsis thaliana TLP11 sequence is the gene is located at chromosome III.
                                                                                                                                                                                                                                                                                                                   117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTCCAGTCGGTCATCACCAGTCTTTAGGTCTCACTCAAAACCATTGCGCAGTAATAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAGAAGCCAAGCTTATGTTGGCAAAGTGAGATCGAAACTTCCTAGGAACGAAATTCACT
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                                                                                                                                                                                                                                                                                                                   GCCGCCGCCTCAACCGCTAATAGTTCAGACCCTTTCAGCTCGGAGCTCCCGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                         CTTCTTAGGGAGATTCTGATTCGTGTTGAAGCGGCGGACGGTGGCGGATGGCCGTCACGA
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New isolated Arabidopsis TUBBY-like proteins, useful for producing transgenic or transformed cells or plants having higher tolerance salt, chilling, pathogens, oxidative stress, or water-deficit.
                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                           Score 567.8; DB 14; Length 1140; Pred. No. 6.3e-176;
                                                                                                                                                                                                                                Seguence 1140 BP; 287 A; 268 C; 288 G; 297 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                       0; Mismatches 252; Indels
                                                        7; SEQ ID NO 22; 43pp; English
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Yu Y; JP, Haas WD; Hoffman N;

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The invention describes an Arabidopsis thaliana mucleic acid (I). The polypeptide (II) encoded by (I), transgenic plant (III) or geneticallly composition (IV) are useful for screening a candidate agent for its biological effect, by combining the candidate agent with (II), (III) or (IV), and determining the effect of the candidate agent on (II), (III) or (IV), and determining the effect of the candidate agent on (II), (III) or (IV), and determining the effect of the candidate agent on (II), (III) or (IV). (I) is useful for identifying homologous or related genes, for producing compositions that modulate the expression or function of its encoded protein, for mapping functional regions of the protein, in changing that calls, in screening assays of various plant strains to determine the strains that are capable of various plant strains to determine the strains that are capable of various production of blosynthetic product in a plant, for producing polypeptides, as probes for the detection of mRNA in biological continuing oligomucleotides, as probes for the detection of mRNA in biological samples, to generate additional copies of (I), to generate ribozymes or oligomucleotides, as single stranded DNA probes or as triple-strand for introducing or improving disease resistance and stress collegant for introducing or improving disease resistance and stress to transgenic organisms, such as plant cells and plants. (II) or (III) is useful as crops for their enhanced diseased resistance, enhanced traites of interest, for screening programs, as crops which exhibit chalance to environmental stress, or to produce a factor. This sequence represents a nucleic acid that may correspond to naturally contained in electronic format directly from the US patent office at sequence. The sequence the print of the printed specification, but was obtained in electronic format directly from the Boguence of sequence.
                                                                                                           Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
                                                                                                                                                                                                                               Claim 1; SEQ ID NO 879; 43pp; English
                                                        WPI; 2003-110411/10.
  Hurban
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Sequence 396 BP; 97 A; 91 C; 89 G; 119 T; 0 U; 0 Other;

339 160 GGCGATTGGCCGTCGCGGCGAAACGTGGTGGCTTGTGCCGGCGTTTGTCGTAGCTGGAGG 219 279 61 ATTCTCACCAAGGAGATTGTAGCTGTTCCTGAATTCTCCTCTAAATTGACTTTCCCTATC 120 121 TCCCTCAAGCAGTCTGGTCCAAGAGATTCTCTAGTTCAATGCTTTATAAAACGTAATCGA 180 AATACTCAATCGTATCATCTCTATCTCGGATTAACTACCTCTTTGACGGATAACGGGAAG 399 181 AATACTCAATCGTATCATCTCTATCTCGGATTAACTACCTCTTTGACGGATAACGGGAAG 240 TTTCTTCTTGCTGCTTCTAAGCTGAAGCGCGCAACTTGCACTGATTACATCATCTTTTG 459 241 Tricricirecrecriciaaecreaaececeaacricacrearracarcarcrire 300 CGTTCAGACGATATCTCAAAGAGAAGCAACGCGTATCTTGGGAGAATGAGATCGAACTTC 519 9 220 ATTCTCAACAAGGAGATTGTAGCTGTTCCTGAATTCTCCTCTAAATTGACTTTCCCTATC GECGATTGECCGTCGCGGCGAAACGTGGTTGGTTGTTGTTGTCGTAGCTGGAGG TCCCTCAAGCAGTCTGGTCCAAGAGATTCTCTAGTTCAATGCTTTATAAAACGTAATCGA Gaps , 0 34.7%; Score 396; DB 8; Length 396; 100.0%; Pred. No. 1.7e-119; ive 0; Mismatches 0; Indels 361 CTTGGAACAAAATTCACGGTCTTTGATGGTAGTCAG 396 CTTGGAACAAATTCACGGTCTTTGATGGTAGTCAG 555 34.78; Best Local Similarity 100. Matches 396; Conservative 280 400 520 Query Match 340 460 셤 ઠે g ઠે 셤 ð 셤 ŝ 셤 ò g δ δ

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285 écecceaceaceaceacearrasecceaecrécrécrésecanames 344 121 CTTAGAGAAATCCTGATTAGGGTTGAGACTGTTGACGGCGGCGGCGATTGGCCGTCGCGGCGA 180 345 crecescagerecresrananica de cercesa --- e de creciede de contra de 101

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This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drough, salt or disease tolerance, height to the plant such as increased drough, salt or disease tolerance, height cutrifional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroms or plant height. This polymucleotide is a plant transcription factor cDNA sequence of the invention.
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                                                                                                                                                                                                                     transgenic plant, drought resistance, disease resistance, salt tolerance, cold tolerance; freezing tolerance, flowering, flavor enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
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Lund ST, Magusin A;
1 C, Gause K, Wood
                                                                                                                                                             Eucalyptus grandis transcription factor cDNA TUBBY family Seq 421
                                                                                                                                                                                                    gene; ss; plant; transcription; gene regulation; gene expression;
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Higgins C, Lasham A, Lund
Veerakone S, Westwood C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; SEQ ID NO 421; 1265pp; English.
                                       ADW16693 standard; cDNA; 1681
                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2004; 2004WO-US017965.
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                                                                                                                     (first entry)
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Forster RLS, Grigor M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ARBO-) ARBORGEN LLC.
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                                                                                                                                                                                                                                                                                                       Eucalyptus grandis.
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                                                                                                                                                                                                                                                                                                                                               WO2005001050-A2.
                                                                                                                                                                                                                                                                   flower color.
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Matches
RESULT 7
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946 ACAGTGGCTTCGGTTAAGAACTTTCAGCTTGTGGCAGTTAGTGACTGTGAA---GCAGGG 1002
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                                                                                                                                     AGAGATTCTCTAGTTCAATGCTTTATAAAACGTAATCGAAATACTCAATCGTATCATCTC
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 AACGTGGTGGCTTGTGCCGGCGTTTGTCGTAGCTGGAGGATTCTCACCAAGGAGATTGTA
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme composing path tolerance to cold, heat, drought, herbicides, extreme plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for monipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one or by providing improved plant growth and sevelopment under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert plant can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 GCTGGTCGGAGCTCCCGGAGGAGCTGCTTAGAGAAATCCTGATTAGGGTTGAGACTGTTG 154
                                                                                                                                       plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; aglactomannan production; light production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 GTTGGGCCAACATGCCCCAAGAGCTTCTCCGAGAGGTCCTCCTCCGAATCGAG---GCCT
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Pred. No. 7.9e-110;
0; Mismatches 367; Indels 26;
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                                                                                                  Plant full length insert polynucleotide seqid 8367.
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05-NOV-2001; 2001US-00985678.
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Best Local Similarity 63.2%;
Matches 674; Conservative
                                                            (first entry)
                                                                                                                                                                                                                                                                                       protein content; gene; ss
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improving yield.
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ADX13792 standard; cDNA; 1629 BP ADX13792 ID ADX1 RESULT 8

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991 GTTGGTGCCTGAACTTTCATGGACGGGTGACAATTGCCTCAGTTAAAAACTTTCAGCTGG 1050
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                                                                                                                                     GGAGGATTCTCACCAAGGAGATTGTAGCTGTTCCTGAATTCTCCTCTAAATTGACTTTCC
                                                                                                                                                                                           GGAGACATATCACCAAAGACATTGTCAAAACGCCCGAACTCTCCTCCAAGATCACTTCC
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   ACGCCGCCGATTGGCCGTCGCGGCGAAACGTGGTGGCTTGTGCGTTTGTCGTAGCT
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This invention relates to novel isolated plant mucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The present cranscription factor that regulates the promoter, which is operably invention describes DNA constructs containing DNA encoding a cranscription factor that regulates the promoter, which is operably linked to the desired mucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait of the plant such as increased drought, salt or disease tolerance, height change, enhanced cold/ frost tolerance, enhanced color, health and cutritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

CC Accordingly, such plants that are successfully transfetced with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, arome or plant height. This polynucleotide is a plant transcription factor cDNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; ss; plant; transcription; gene regulation; gene expression; transgenic plant; drought resistance; disease resistance; salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides isolated from plants encoding transcription factors, polypeptides encoded by such polynucleotides, useful for regulating transcription and gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connett MB, Emerson SJ, Frost MJ;
Higgins C, Lasham A, Lund ST, Magusin A;
Veerakone S, Westwood C, Gause K, Wood
                                                                                               Eucalyptus grandis transcription factor cDNA TUBBY family Seq 422
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                                                                                                                                                                                                                                                                                                                                                                  07-JUN-2004; 2004WO-US017965.
                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-2003; 2003US-0476189P
                                                         (first entry)
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Matches 677; Conservative
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Forster RLS, Grigor M,
Phillips J, Puthigae S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ARBO-) ARBORGEN LLC.
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                   ADW16694;
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1. 1218 /*tag= a /product= "Arabidopsis thaliana TLP3 protein"

Location/Qualifiers

/note= "No stop codon"

/partial

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New isolated Arabidopsis TUBBY-like proteins, useful for producing transgenic or transformed cells or plants having higher tolerance tsalt, chilling, pathogens, oxidative stress, or water-deficit.
                     Transgenic plant; salt tolerance; crop improvement; cold toleranc oxidative stress; drought resistance; TUBBY-like protein; plant; chromosome 2; gene; ss.
Arabidopsis thaliana TUBBY-like protein (TLP) 3 encoding
                                                                                                                                                                                                                                                 21-JAN-2004; 2004US-00763042.
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                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-080955/09.
P-PSDB; ADW64857.
GENBANK; AY045774.
                                                                                                                                                                                                                                                                                                     (SINI-) ACAD SINICA
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                                                     The invention relates to Arabidopsis TUBBY-like proteins (TLP) and their corresponding nucleic acid sequences. The invention also relates to a transformed cell or a transgenic plant containing TLP nucleic acid and a transformed cell or a transgenic plant lacking TLP nucleic acid. The polypeptides and nucleic acids are useful for producing transgenic or transformed cells or plants having higher tolerance to salt, chilling, pathogens, oxidative stress or water-deficit. The present sequence is the Arabidopsis thaliana TLP3 encoding cDNA. The Arabidopsis thaliana TLP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 30.1%; Score 342.6; DB 14; Length 1218; I Similarity 59.8%; Pred. No. 1.4e-101; Conservative 0; Mismatches 429; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1218 BP; 320 A; 297 C; 283 G; 318 T; 0 U; 0 Other;
Claim 7; SEQ ID NO 14; 43pp; English
                                                                                                                                                                                                                                                                                                                                                gene is located at chromosome II
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BP

CDNA; 1218

ADW64868 standard;

(first entry)

07-APR-2005

ADW64868;

RESULT 10
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                         GaAACCGCAGCAATCAACCTACTATCTATACCTCGGGTTAAACCAAGCAGCTTCAAATG
                                                     ATAACGGGAAGTTTCTTCTTGCTGCTTCTAAGCTGAAGCGCGCAACTTGCACTGATTACA
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Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1299
                                                                                                                          gene; 88; plant; transgenic; B2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism
                           ADN73404 standard; cDNA; 1221 BP
                                                                            (first entry)
                                                                                                                                                                                Arabidopsis thaliana
                                                                           15-JUL-2004
                                                    ADN73404;
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up convencentiated in transgenic plants overexpressing the heterodimeric STR-JDPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, carying plants for the production of growth regulators, carymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal rachitecture or physiology, attered endoreduplication, biochemistry, signal architecture or physiology, attered endoreduplication, biochemistry, signal architecture can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell wall biosynthesis, introgen and/or carbon meterabolism or they function as transcription factors. This polymuclectide sequence is thale creas CDNA uranscription factor, given in an exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                              Altering plant characteristics, useful for producing plants for enzyme cpharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
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29-APR-2004
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The invention relates to a novel DNA sequence encoding a transcription factor derived from a plant. The invention further comprises antisense RNA sequences, ribozyme activity RNA, RNA sequences, a vector.

C transformed plant cells, antibodies and proteins, all related to the carried from a rice-genome database. The invention further provides a method for determining the transcription regulatory regions of the rice genome. The novel DNA is useful for controlling the expression of a gene in a plant and for producing a modified plant with desired and different characteristics. The plant DNA and method enables the acquisition of many cranscriptional-regulatory regions. This polymucleotide represents a DNA sequence taken from a rice genome clone library for use in the invention. Note: This sequence is not shown in the specification. It has been retrieved from a sequence listing in electronic format from the Japanese Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to 28469 and encoded protein sequences of SEQ ID Nos 28470 to 56791.
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Kishimoto N, Sato K, Nagata T, Kawakami N, Yazaki J, Ishikawa
Doi K, Kawai J;
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel DNA encoding transcription factor, derived from rice plant, for obtaining transcriptional-regulatory regions in plant and for producing modified plant.
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                                                               (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH. (SBRIB-) SEBIBUTSUKEI TOKUTEI SANGYO GIJUTSU. (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH. (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZALIDAN.
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30-MAY-2002; 2002JP-00203269.
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                                                                                                                                         741 AGTAGTAGCTTCAACATCCATAAGCTCTTTTTCCAGTCGGTCATCACCAGTCTTTAGGTC
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                                                                                                                                                                                                                   861 AGATCCACCATTGGTGCTGAGCAACAAAGCTCCACGGTGGCATGAGCAGTTACGTTG
                             ----CGAAGATGCAGAAGAGCCGCTCTTCTAATTTCATCAAAGTTTCACCTAGAGTTCC
                                              GATTTCAAAGGGTCAGTCTGCACGTGGTTGGTTCAAACCATTTATCCCCCAGGATACC
                                                                  TCAGGGAAGTTACCCCATCGCTCACATTTCATACGAGTTAAACGTCTTAGGCTCTCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana nucleic acid sequence Ref:2027216 SEQ ID NO:216.
                                                                                                                                                                                                                                                                                                                                                                     1098 TGCTATCTGCCTGAGCAGTTTTGAAACCAGAATTGCCTGTGAA 1140
                                                                                                                                                                                                                                                                                                                                                                                ABL93451 standard; cDNA; 469 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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HAMILTON C M.
PRICE J L.
RAINES T M.
YU Y.

(ANYY/) (HAMI/) (PRIC/) (RAIN/) (YUYY/)

GORLACH J.

GORL/)

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The present invention describes an Arabidophia functional functions of the greater and the sequence capable of phybridising under stringent conditions to a sequence (S1) selected from any one of the 999 sequences given in ABL93236 to ABL94234. (I) have insecticide and functions and the sequences given in they can be used as protein expression modulators. (I) can be used in identifying homologous or related genes, in producing compositions that identifying homologous or related genes, in producing compositions that compositions that it is marginate the expression or function of their encoded proteins, mapping functional regions of the proteins, and in studying associated physiological pathways. (I) can also be used: (I) for the genetic physiological pathways. (I) can also be used: (I) for the genetic of witherious plate strains to determine the strains that are best capable of various plant strains to determine the strains that are best capable of witheranding a particular disease or environmental stress; (3) for enhancing or inhibiting production of a biosynthetic product in a plant; (A) as probes in mapping and in diagnosis, in genetic modification and for screening purposes, to generate additional copies of the nucleic acids, to generate ribozymes or antisense oligonucleotides, and as single for generating genetically modified transgenic organisms. Note: The sequence data for this patent did not form part of the printed regenerate specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologous genes,
function of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an Arabidopsis thaliana nucleic acid (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 AAGCAGGCAACATCTGAGAGGATCATACTCCAGTTTGGGAAAGTTGGGAAGGACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      815 TGCGCAGTAATAGTGCATCATGTAGCGACTCAGGCAACAACCTGGGAGATCCACCATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 TGCTGAGCAAAAACTCCACGGTGGCATGAGCAGTTACGTTGCTGCTGGTGCTTAAATTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Haas WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      JP, Haas Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Arabidopsis thaliana nucleic acid, for identifying homologous producing compositions that modulate the expression or function of encoded protein, and mapping functional regions of a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 469 BP; 133 A; 116 C; 90 G; 130 T; 0 U; 0 Other;
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Ledford BL, Woessner
Davis KR, Allen K,
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100.0%; Pred. No. 2.4e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 216; 44pp; English.
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Page A, Mathew AV,
Kricker M, Slater T,
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Matches 326; Conservative
                                                     MATHEW A V.
LEDFORD B L.
WOESSNER J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-267486/31.
RAMEAKA J G.
                                                                                                                                            HAAS W D.
GARCIA C A.
                                                                                                                                                                                                  KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
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Rameaka JG,
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Hurban P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Plnus radiata. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait co the plant such as increased drought, salt or disease tolerance, height change, enhanced cold, frost tolerance, enhanced color, health and nutritional characteristics, as well as improved taste, starch
  TTACCATGGATTATGGATATCCGATTTCTGCGTTTCAAGCGTTTGCTATCTGCCTGAGCA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene, ss, plant, transcription, gene regulation, gene expression, transgenic plant, drought resistance, disease resistance, salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             petal or
is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    composition, flower longevity and germination, amongst others. Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal leaf shape and size, arom or plant height. This polymuclectide is a plant transcription factor cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connett MB, Emerson SJ, Frost MJ;
Higgins C, Lasham A, Lund ST, Magusin.
Veerakone S, Westwood C, Gause K, Woo
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                                                                                                                                                                                                                                                                                                                                                                                                Pinus radiata transcription factor cDNA TUBBY family Seg 808.
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                                                      GITTIGAAACCAGAAITGCCTGTGAA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 808; 1265pp; English.
                                                                               ADW17065 standard; cDNA; 1887 BP
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                                                                                                                                                                                                                                                                                                                                               (first entry)
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Forster RLS, Grigor M,
Phillips J, Puthigae S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ARBO-) ARBORGEN LLC
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ADM17065
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                                                                                            ATATTATTGAGAATTGAGAGCAGCGAGATCACC---TGGCCTGCACGGAGGAACGTTG
                                                                                                                                                                                                                                                                                                                 769 TGGTTTGTGCTGCCGTGTGCAGAACGTGGAGGGAAATTATCAAGGAGATTGTGAAACCGC
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     AAATCCTGATTAGGGTTGAAGACTGTTGACGGCGGCGATTGGCCGTCGCGGCGAAACGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAATTCTCCTCTAAATTGACTTTCCCTATCTCCCTCAAGCAGTCTGGTCCAAGAGATT
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Local Similatio, nes 656; Conservative

Matches

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5

Gaps

us-10-763-042-20.rng

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This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Bucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably inked to the desired nucleic acid to be expressed. It further provides transcription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides to the plant such as increased drought, salt or disease tolerance, height cother plants that are successfully transfected with a DNA composition, flower longevity and germination, amongst others.

Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polymucleotide is a plant transcription factor cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                     gene; ss; plant; transcription; gene regulation; gene expression; transgenic plant; drought resistance; disease resistance; salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer; flower color.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynuclectides isolated from plants encoding transcription factors, and polypeptides encoded by such polynuclectides, useful for regulating gene transcription and gene expression.
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Higgins C, Lasham A, Lund ST, Magusin A;
Veerakone S, Westwood C, Gause K, Wood
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Pred. No. 1.1e-94;
0; Mismatches 400; Indels 39
                                                                                                                                                                                                                                                                      Pinus radiata transcription factor cDNA TUBBY family Seq 809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1923 BP; 514 A; 374 C; 457 G; 578 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 809; 1265pp; English
                                           ADW17066 standard; cDNA; 1923 BP
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                                                                                                                                                                                            (first entry)
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Forster RLS, Grigor M,
Phillips J, Puthigae S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641; Conservative
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                                                                                                                     ADW17066;
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ADWI7066

IND ADWI7066

XXX ADWI7066

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Identification of novel e2f target genes and
Patent: WO 2004035798-A 943 29-APR-2004;
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Arabidopsis thaliana Bukaryota; Embryophyta; Tracheophyta; Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (Dases 1 to 1143)
Lai, C. P., Lee, C. L., Chen, P. H., Wu, S. H., Yang, C. C. and Shaw, J. F. Molecular Analyses of the Arabidopsis TUBBY-Like Protein Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCGGCTCAACCGCTAATAGTTCAGACCCTTTCAGCTGGTCGGAGCTCCCGGAGGAGCTG
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Lai, C.P. and Shaw, J.F.

Cloning and characterization of cDNAs for tubby-like p

Unpublished

3 (Dases I to 1143)

Lai, C.P. and Shaw, J.F.

Direct Submission

Submitted (25-FEB-2002) Institute of Botany, Academia Submitted (25-FEB-2002)

Nankang, Italpei, Talwan 11529, Republic of China

Location/Qualifiers
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Arabidopsis thaliana (thale cress)

AF487270.1 GI:33320970

ACCESSION VERSION KEYWORDS SOURCE

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Yamada, K., Chan, M. M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodeas, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., WH.C., Yu, G., Yuan, S., Quach, H.L., Tang, C.C., Toriumi, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
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147. .1380
/gene="At3g06380"
/gene="At3g06380"
/note="This is a potential full length cDNA corresponding to At3g06380 and may be the product of a partially processed transcript."
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAS: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.
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/note="compared to genomic sequence"
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fectype="Columbia"
/note="This clone is m a modified
(lambda PS) as a BamHI/XhoI insert.
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/organisma-Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="3"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; eurosida II; Brassicales; Brassicacea; Arabidopsis.

1 (bases 1 to 1595)
Syamada, K., Chan, M.M., Chan, M., Heuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, K., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Arabidopsis Full Length cDNA Clones
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W.html), and NerPlantGene ne.html), searches of the ase and the Arabidopsis ('tdb/at/at.html). ! level of evidence for o other proteins are named gnificant peptide med as 'unknown' proteins. that are predicted by more set of their length are Masker.html). Regions of genes but have predicted es. linear PLN 30-OCT-2002 some III and is near the oryophyta; Tracheophyta; ns; core eudicotyledons; seae; Arabidopsis. reasy, T.H., Haas, B., c, T.R., Barnstead, M.E., nser, C.M. HPI7 genomic sequence to T7 end of the BAC three methods: Gene lble by anonymous ftp Green, University of Jenomic Research, 9712
A, xlin@tigr.org denomic Research, 9712 Simple repeats are јА aced gi:12280803.

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/note="similar to putative Anion exchanger family members:
GB:AAD39673, GB:AAD55295 [Arabidopsis thaliana]"
join(212993. 13102,13175. 13257,13357. 13549,13667. 13805,
13900. 14065,14182. 14339,14418. 14612,14700. 14795,
14879. 15013,15093. 15400,15493. 115763,15855. .>16211)
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REHALCEPROVVENDELFERAQUPELSKILEKEDES DITLLILGESS LOKELSE HAVEHAT
RVYMCYLMIKTROSHEP LALVINSTYHVINYGYYFLCAVGSREWMKLUYDCGIVGFY
FSFGLSGWMLREHLFGSGCTGIWGWCFNAAFNASLLALFSNFHSKNYVKKPTREDGKK
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Thote="exon predicted by xgrail, quality good_shadowexon"

complement(10146. .11457)

/gene="F24P17.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55852 GCCGCCTCAACCGCTAATAGTTCAGACCCTTTCAGGTGGTCGGAGGTCCCCGGAGGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AACGTGGTGGTCGCCCCCCCTTTGTCGTAGCTGGAGGATTCTCACCAAGGAGATTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGACGTTCCGAAGTTTACTCCAGGAAATGCGGTCTAGGCCACACCGTGTAGTTCACGCC
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complement (8719. .9615)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (<8719. .>9615)
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Matches 1140; Conservative
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LPRIFTYLYSTARNPLEEDVDLGIADVPVTMAGYGYGLPISRLYARYFGGDLQIISME
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VI I FCSTKRLCDHLARSVGRHPGAVVIHGDKTOGERDWVLNOFRSGKSCVLIATDVAA
RGLDIKDIRVVINYDPPTGVEDYVHRIGRTGRAGATGVAFTFFTEQDWKYAPDILKVU
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RSRSRSGSYSRSRSRSSSSRSRSRSPRSFSRSPPHSRDRGGHNRSRSYSRSPSPVYERRDRAPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to RNA helicase (DRH1) GB:BAA28347 [Azabidopats thalianal; Pfam HMW hits: WW/rsp5/WWP domain containing proteins, DBAD and DBAH box helicases, Helicases conserved C-terminal domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (2022. .2051)
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excellent shadowexon"
2057. .2160
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                                                                                                                                                                                                                                                partial"
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                1000 rereccacieccacedearercacedadadescadaeceaecedarrarararecaerri 1059
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Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R.
Direct Submission
Submitted (27-NOV-2003) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1259)
Cheuk,R., Chen,H., Kim,C.J., Shinn,P. and Ecker,J.R.
Unpublished
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                                                                                                                                           1120 GCTTTTGCCATTTGCTTGAGCAGCTTTGAGACTAGAATCGCTTGTGAA 1167
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/mol_type="mRNA"
/db_xref="taxon:3702"
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/translation="MRSRPHRVVHDLAAAAADSTSVSSODYRWSEIPEELLREILIR VEAADGGGWPSRRSVVACAGVCRGWRLLANBITVVVPBISSKLTFPISLKQPGPRDSLV OVETRRNRITGSYHLYLGITNSLTDDGKFLLAACKSHTTCTDYIISLRSDDMSRRSQ AYGYKVRSNRITGTKFTPONLLPSTAAKLRKSRSYNPAKVSAKVPLGSYPAHITY ELNYLGSRGPRAWQCLMDTIPPSTMBPQGVASBPSBFPLGTRSTLSRSQSKPHRSSS SHLKETPLVLSNKTPRWHEQLRCWCLNFHGRVTVASVKNFQLVAAGASCGSGTGMSPE PLN 15-APR-2004 228 297 288 357 348 417 408 477 468 478 AAGAGAAGCAACGCGTATCTTGGGAGAATGAGATCGAACTTCCTTGGAACAAAATTCACG 537 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1143)
Lai, C.P., Lee, C.L., Chen, P.H., Wu, S.H., Yang, C.C. and Shaw, J.F. Molecular Analyses of the Arabidopsis TUBBY-Like Protein Gene GCCGCCGCCTCAACCCGCTAATAGTTCAGACCCTTTCAGCTCGGAGCTCCCCGGAGGAG 117 108 177 237 289 CCAAGGGATTCACTGGTTCAATGCTTTATCAAACGTAATCGAATTACGCAATCATT CTGCTTAGAGAAATCCTGATTAGGGTTGAGACTGTTGACGCGGCGGTTGGCCGTCGCGG CGAAACGTGGCTTGTGCCGGCGTTTGTCGTAGCTGGAGGATTCTCACCAAGGAGATT ércérrércercia de l'entre de l CCAAGAGATTCTCTAGTTCAATGCTTTATAAAACGTAATCGAAATACTCAATCGTATCAT CICTATCICGGAITAACIACCICITIGACGGAATAACGGGAAGITICITCITCITGCIGCITCI 349 cicialcicedarnaaccaacicritaacedarearededaacitritecirectecerer AAGCTGAAGCGCGCAACTTGCACTGATTACATCTCTTTGCGTTCAGACGATATCTCA GCTGCCCGATTCCACTTCTGTCATCGCAAGATTATCGCTGGTCAGAGATTCCTGAAGAG GTAGCTGTTCCTGAATTCTCCTCTAAATTGACTTTCCCTATCTCCCTCAAGCAGTCTGGT Gaps mRNA linear PLN 15-API protein 12 mRNA, complete cds Lai, C.P. and Shaw, J.F.
Direct Submission
Submitted (18-JUI-2001) Institute of Botany, Academia Sinica, Nankang, Taipei, Taiwan 11529, Republic of China
Location/Qualifiers 51; RQSERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE" Length 1143; Indels 49.8%; Score 567.8; DB 15; 72.8%; Pred. No. 1.1e-172; iive 0; Mismatches 252; 1. .1143 /organiam="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /product="tubby-like protein 12" /protein_id="AAL03978.1" /db_xref="G1:37542296" Family Plant Physiol. 134 (4), 1586-1597 (2004) cress) Arabidopsis thaliana tubby-like AYO46922 Arabidopsis thaliana (thale GI:37542295 codon_start=1 g ò

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                                                  Length 1781;
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                                                     DB 15;
                                                  Score 350.6; DB 15;
Pred. No. 6.1e-102;
0; Mismatches 449;
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Best Local Similarity 59.2%;
Matches 678; Conservative
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    (Dases 1 to 1221)

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Molecular Analyses of the Arabidopsis TUBBY-Like Protein Gene
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Lai.C.P. and Shaw,J.F.
Direct Submission
Submitted (16-UUL-2001) Institute of Botany, Academia Sinica,
Nankang, Taipei, Taiwan 11529, Republic of China
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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   GGATCATACTCCAGTTTGGGAAAGTTGGGAAGGACATGTTTACCATGGATTATGGATATC
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                                                                                                                            CGATTTCTGCGTTTCAAGCGTTTGCTATCTGCCTGAGCAGTTTTGAAACCAGAATTGCCT
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Identification of novel e2f target genes and use thereof
Patent: WO 2004035798-A 1299 29-APR-2004;
CropDesign N.V. (BE)
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Pred. No. 2.4e-99;
0; Mismatches 429;
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1221 bp DNA
Sequence 1299 from Patent WO2004035798.
CQ804888
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1 (Dates 1 to 1252)

Yamada, K. Banh, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Deng, J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satcu, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R. W., Eckr, J. R., and Theologis, A. Arabidopsis Open Reading Frame (ORF) Clones

L. Unpublished

L. Jases I to 1252)

Yamada, K., Banh, J., Chan, M. M., Chang, C. H., Chang, B., Dale, J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Shinozaki, K., Davis, R. W., Bcker, J. R. and Theologis, A. Shinozaki, K., Davis, R. W., Bcker, J. R. and Theologis, A. Bundaritted (L. And. And. Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carning Carnin
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Spermatophyta, Magnoliophyta, eudicctyledons; core eudicctyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K.,
                                                                                                                                                                                                                                                                                                                                                                                                      806 GAĞGAACAĞCTCCAACTCAGACGGAACTTGTCCATAGCAATCTTGATAGTTTCCCCTCAT
                                                                                                                      TCTTTAGGTCTCACTCAAAACCATTGCGCAGTAATAGTGCATCATGTAGCGACTCAGGCA
                                                                                                                                                                           866 TCTCCTTCTTCAGGTCGAAATCAATTCGTGCAGAGAGTCTCCCTTCTGGTCCATCATCTG
                                                                                                                                                                                                                                   851 ACAACCTGGGAGATCCACCATTGGTGCTGAGCAACAAAGCTCCACGGTGGCATGAGCAGT
                                                                                                                                                                                                                                                                                     911 TACGTTGCTGGTGCTTAAATTTCCATGGTCGAGTCACAGAGTGGCTTCGGTTAAGAACTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 971 AGCTIGIGGCAGTIAGTGACTGTGAA---GCAGGGCAGACATCTGAGAGGATCATACTCC
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The RIKEN Genomic Sciences Center (GSC) members carried out
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Arabidopsis thaliana putative tubby protein (At2g47900)
   GAGGAGTAGTAGCTTCAACATCCATAAGCTCTTTTCCAGTC
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DAPKQSCWASMPPELLANDLARIEQSBTFWPSRXVVSCAGCRUMRETYREIVRVPE
LSSKLTFPISLKQPGPRGSLIQOVCYIMMENSOTYYLYLGLNQACRUMRETYREIVRVPB
LSSKLTFPISLKQDPGRGSLYOCYIMMENSOTYYLYLGLNQACRUMGFFFLAAKR
RRPTCTDYIISLNCDDVSRGSNTYIGKLRSNFLGTKFTVVDAQPTNPGTQVTRTRSSR
LLLSLKQVPSRIPSGYPTAHISYELNVLGSRGPRRMQCVMDAIPRASMSTRGTATOT
RLLASLKQVPSRIPSGYSTRSKSITSALSPSPAAQUEGLLVLKNKAPRWHEQLGCWCL
NFNGRYLDSPSFSFSFSKSTRSKSTRANDLOFGRANGKEGLLVLKNKAPRWHEGLGCWCL
NFNGRYTVASVKNFQLVAAPENGPAGPBHENVILQFGKVGKOVFTWDYQYPISAPQAR
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                                                                                                                                                                                 protein"
                                              /organism="Arabidopsis thaliana"
/mol_type="mRNA"
                                                                                                                                                                                                                                /product="tubby-like protein 3"
/protein_id="AAK98802.1"
/db_xref="GI:27372514"
                                                                                                                                                                              /note="putative Tub family
                                                                                                                xref="taxon:3702"
Location/Qualifiers
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18-SEP-2002 mRNA,

Ishida, J.,

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FLI CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1943)

Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,

Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,

Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,

Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,

Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,

Satou,M., Seki,M., Schinn,P., Southwick,A., Shinozaki,K.,

Davis, R.W., Ecker,J.R. and Theologis,A., Shinozaki,K.,

Arabidopsis Full Length cDNA Clones
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DAFKGSCWASWPPELLRDVLAKIEQSEDTWPSRVNVSGGGCVRNWREIST VKEIVRVPE
LSKTLFPISLKQPGRGSLIVQCYINRNRSNOTYYLYLGLNQACSNDGKFLLAARR
RSPTCTPIISLKQPGRGSLIVQCYINRNRSNFLGTKFTVYDAQPTNPGTQVTRTRSSR
ELLSLKQVPSRTISGMYPVAHISYELNTGRENSPRMQCWDAATPASPRGGTAPTQT
ELLSLKQVPSRTISGNYPVAHISYELNTGRENSPRMQCWDAATPASPRSGGTAPTQT
RINGNYNSULDSPSPSPSPSRSIFASELSGGSSAAQKEGLLVLKNKAPRWHEGLGCWGT
NFORRYTVASVKNFQLVAAPENGPRGFBENVILLQFGKVGKDVFTMDYQYPISAFQAF
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                                                                                                                                                                                                                                                               Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 GATCCAGGTCTCAACGTGTTGTTCAGGATACTTCTGTTCCTGTTGATGCTTTCAAGCAGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 TCAGCTGGTCGGAGCTCCCGGAGGAGCTGCTTAGAGAAATCCTGATTAGGGTTGAGACTG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 acrigocgagaaricgrcaagagarcgrcagagrrccrgagcrrrrcragcaaacrcacrr 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCCTATCTCCCTCAAGCAGTCTGGTCCAAGAGATTCTCTAGTTCAATGCTTTATAAAAC 331
                                                                                                                                                                    Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
  Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriuni, M., Wu, H.C., Yamamura, Y., Yu, G., Bowesr, L., Chen, H., Cheuk, R., Jones, Y. Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
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Pred. No. 2.4e-99;
0; Mismatches 429; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative tubby protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=experimental
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                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome="2"
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11 Similarity 59.8%;
677; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product = putative tubby protein"
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RUNNSNLDSFPSFSFFRSKSITASFELNULGFGKVGKDVFTMDYQYPISAFQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t
                                                                                                                                                                                                                                   Submitted (11-JNN-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the Collection and clustering of RAPL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                              Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Yu, G., Bowser, L.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Mayers, M. C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                   The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /ecotype="Columbia"
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(FLC-1) as a BamHI/XhoI insert."
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30.1%; Score 342.6; DB 15; Length 1943;
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Matches 677; Conservative 0; Mismatches 429; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Arabidopsis thaliana"
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                    REFERENCE
AUTHORS
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GGTCTAGGCCACACCGTGTAGTTCACGCCGCCGCCTCAACGCCGTAATAGTTCAGACCCTT

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1019 1319 1439 1499 1027 1559 1087 1619 .080 CTCAGGTTACCAGAACCCGTTCAAGCAGACTTCTCAGTTTGAAACAAGTGAGCCCGAGAA 1139 1140 TTCCATCTGGCAACTATCCTGTAGCACATATCTCATATGAGCTTAACGTCTTGGGTTCCA 1199 1200 GAGGACCGAGGAAGGAAGGAGGTGTCATGGATGCCATCCCTGCATCAGCTGTAGAACCTG 1259 1320 TCTCCTTCTTCAGGTCGAATCAATTCGTGCAGAGTCTCCCTTCTGGTCCATCATCTG 1379 910 565 448 508 919 790 970 662 211 719 271 779 839 388 899 959 TCCCTATCTCCCTCAAGCAGTCTGGTCCAAGAGATTCTCTAGTTCAATGCTTTATAAAAC 331 92 TCAGCTGGTCGGAGCTCCCGGAGGAGCTGCTTAGAGAAATCCTGATTAGGGTTGAGACTG 603 GCTGCTGGGCTAGTATGCCTCCGGAGCTCCTGAGAGATGTTCTTATGAGGATTGAGCAAT 663 CCGAAGACAC---TTGGCCGTCTAGGAAAAATGTTGTTTCTTGCGCTGGTGTCTGCAGGA 780 TTCCTATCTCCCTCAAACAGCCGGGTCCTAGAGGATCACTTGTTCAATGCTATATTGA GAAACCGCAGCAATCAAACCTACTATACTCGGGTTAAACCAAGCAGCTTCAAATG 900 ATGATGGAAAGTTCCTTCTTGCTGCCAAGAGGTTTCGGAGGCCAACTTGCACTGACTACA 212 GCTGGAGGATTCTCACCAAGGAGATTGTAGCTGTTCCTGAATTCTCCTCTAAATTGACTT 720 ACTGGCGAGAAATCGTCAAAGAGATCGTCAGAGTTCCTGAGCTTTCTAGCAAACTCACTT 332 GTAATCGAAATACTCAATCGTATCATCTCTCTCGCATTAA---CTACCTCTTTGACGG ATAACGGGAAGTTTCTTCTTGCTGCTTCTAAGCTGAAGCGCGCAACTTGCACTGATTACA 449 TCATCTCTTTGCGTTCAGACGATATCTCAAAGAGAAGGAACGCGTATCTTGGGAGAATGA 960 TCATCTCTTTAAACTGCGATGATGTCTCTCTGAGGAAGCAATACCTATATCGGAAAGCTTA GATCGAACTTCCTTGGAACAAATTCACGGTCTTTGATGGTAGTCAGACCGGAGCAG--------CGAAGATGCAGAAGAGCCGCTCTTCTAATTTCATCAAAGTTTCACCTAGAG TICCICAGGGAAGTIACCCCATCGCTCACATTICATACGAGTTAAACGTCTTAGGCTCTC GGGGACCGAGAAGAATGCGTTGCATCATGGATACAATACCTATGAGCATCGTGGAGTCGC GAGGAGTAGTAGCTTCAACATCCATAAGCTCTTTTTCCAGTC-----GGTCATCACCAG 1260 GAGGAACAGCTCCAACTCAGACGGAACTTGTCCATAGCAATCTTGATAGTTTCCCCTCAT TCTTTAGGTCTCACTCAAAACCATTGCGCAGTAATAGTGCATCATGTAGCGACTCAGGCA 851 ACAACCTGGGAGATCCACCATTGGTGCTGAGCAACAAAGCTCCACGGTGGCATGAGCAGT 1380 crecrcagaaggaaggacrecrcrcrcagaaaaacaaacccccagarcccacaaacac 911 TACGTTGCTGGTGCTTAAATTTCCATGGTCGAGTCACAGTGGCTTCGGTTAAGAACTTTC 1440 TCCAGTGCTGCTGCACTTCAATGGGAGAGTCACAGTTGCTTCCGTCAAAAACTTTC 971 AGCITGIGGCAGTIAGTGACTGTGAA---GCAGGGCAGACATCTGAGAGGATCATACTCC 152 TTGACGGCGCCGATTGGCCGTCGCGCGAAACGTGGTGGCTTGTGCCCGGCGTTTGTCGTA 1028 AGTTTGGGAAAGTTGGGAAGGACATGTTTACCATGGATTATGGATATCCGATTTCTGCGT 1560 AGTTTGGAAAAGTCGGAAAAGATGTGTTCACAATGGATTATCAGTACCCTATCTCTGCCT 1500 AGCTGGTAGCTGCTCCTGAGAATGGACCTGCAGGACCTGAGCACGAAAACGTGATTCTCC 1088 ITCAAGCGTTTGCTATCTGCCTGAGCAGTTTTGAAACCAGAATTGCCTGTGAA 1140 1620 TCCAGGCCTTCACCATTTGCCTCAGCAGTTTCGACACCCAAGATAGCATGTGAA 1672

SOURCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi, S., Satob, K., Magata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishiawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Coundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imchani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oca, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sasaki, D., Sasato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                    ARNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J023078015, full
insert sequence.
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Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
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                                                                                                                                                                                                                    AKO71159.1 GI:32981182
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantes, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Rodama,T., Ruceaki,T., Kusumegi,T., Lu,M., Manda,M., Kobayashi,M., Rodama,T., Rurseaki,T., Kusumegi,T., Lu,M., Manda,J., Mizuno,K., Marikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,R. Genome Exploration Research Group in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hapilzume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiramoto,K., Hiramoto,T., Kagawa,T., Kanagawa,S., Katch,H., Kawai,J., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Koya,S., Kutihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Nimasaki,R., Ohno,M., Osato,N., Ota,Y., Satoh,H., Sakai,C., Sakai,K., Shinagawa,A., Shiraki,T., Sasaki,D., Sato,K., Shinagawa,A., Shiraki,T., Takaku-Akahira,S., Tanama,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
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Best Local Similarity
Matches 632; Conserv
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VILL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashiran, Doi, W., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T. and
Yamamclo, M.
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Rujimura, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
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Sugiyama, A., Suzuki, Y., Tannoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
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Kishikawa Hirozane, T., Kanagawa, S., Katoh, H., Kawai, J.,
Kaya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
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Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
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Numasaki,R., Ohmeda,R., Nikura,J., Nishi,K., Nomura,K.,
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Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,Y., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Taunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007, Tankuba, Tel:81-29-838-7007, Fax:81-29-838-7007,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521
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Pred. No. 3e-
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Best Local Similarity 59.5%;
Matches 632; Conservative (
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Direct Submission
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FLI_CDNA; oligo-capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Oryza sativa (japonica cultivar-group) cDNA clone:J033091L01, full insert sequence.

RESULT 15 AK102370 LOCUS DEFINITION AK102370.1 GI:32987579 FLI CDNA; CAP trapper. Oryza sativa (japonica cultivar-group)

ACCESSION VERSION KEYWORDS SOURCE

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Spermacophyta Magnoliophyta, illiopsida, Pooles, Portse, Pracheophyta, Spermacophyta, Spermacophyta, Stringiplanes, Streeping, Stringiplanes, Streeping, Stringiplanes, Streeping, Stringiplanes, Streeping, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplanes, Stringiplan
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2, Appli 2, Appli 2, Appli 430, App 357, App 161, App

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Sequence 174, App

Sequence Sequence

Run on:

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APPLICANT: JULI-ICAN NOZL
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: PHOSPHATASE
FILE REFREENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT PILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/189,590
PRIOR PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/189,322
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Publication No. US20050250144A1
GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koji Hayashi
Kaoru Otsuka
Jun-Ichi Yamamoto
Shizuko Ishii
Tomoyasu Sugiyama
Ai Wakamatsu
Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Punahashi
Chiaki Senoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
FILE REFERENCE: 3554,104
CURRENT APPLICATION NUMBER: US/11/172,145
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CURRENT FILING DATE: 2005-06-30
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FRIOR PELLING DATE: 2004-06-30
FRIOR PELLING DATE: 2003-08-15
FRIOR PAPLICATION NUMBER: 0/404,356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 CFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASKLKR-----ATCTDYIISLRSDDIS- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 --KRSNAYLGRMRSNFLGTKFTVFDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHIS 217
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                                    315 VTVASVKNPQLVAVSDCEAGQTSE 338
                                                                             400 STIASLS----TSVSTSESGSTSE 419
                                                                                                                                                                                                                                                  US-11-172-145-10
; Sequence 10, Application US/11172145
; Publication No. US20050272696A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 YELNVLGS 225
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US-11-045-802-30
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Best Local S:
Matches 51
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                                                                                                                                               77 KEIVAVPEFSSK-LTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFL 135
                                                                                                                                                                                           136 LAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGT--KFTVFDGSQTGAAKMQK 193
                                                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDTIPMS------IVESRGVVASTSISSFSSRSSPVFRSH------S 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604 MCKYQLSPTVNMPQDDTVIIEDDRLPVLPPHLSDQSSSS----SHDDVGFVTADAGTWA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      659 KAAISDSADCSLSPD--VDPVLAFQREG------FGRQT----DETKLNTVD 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 SSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASK-LKRA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 RVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 ----GS-----VSTSASLSGSESBSDSQ----SISTSASESTSESASTSLSDSTSTSNSG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 FRSHSKPLRSNSASCSD---SGNNLGDPPLVLSNKAPRWHEQLRCWCLN-----FHGR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 SASTSTSL-SNSASASESDLSSTSLSDSTSA-SMQSSESDSQSTSASLSDSLSTSTSNRM 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 KPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVS 329
Query Match
4.3%; Score 84.5; DB 7; Length 865;
Best Local Similarity 24.1%; Pred. No. 1.9;
Matches 75; Conservative 39; Mismatches 110; Indels 87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 STSMSISMSQSTSGSTSTSTSTSLSDSTSTS----LSLSASMNQSGVDSNSASQSASNS
                                                                                                                                                                                                                                                                                                                                                                                                                               SR---SSNFIKVSPRVPQG-----SYPIAHISYE----LNVLGSRGPRRMRCI
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44; Mismatches 108; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 252, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Gester, Simon
APPLICANT: Foster, Simon
TITLE OF INVENTION: Antigenic Polypeptides
TITLE OF INVENTION: Antigenic Polypeptides
FILE REPERENCE: PloO629W0
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR FILING DATE: 2001-08-02
PRIOR PLING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 424
SEQ ID NOS: 424
SEQ ID NOS: 424
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4.2%; Score 82.5;
Best Local Similarity 23.9%; Pred. No. 2.
Matches 63; Conservative 44; Mismatche
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; ORGANISM: Staphylococcus aureus
US-10-485-517-252
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330 LKEIPSFPR--IHDALPISKEMSKLSNPKIP-----VYINICSI-----PSRIKQLQYT 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 AGV----CRSWRILLTKEIVAVPERSSKLIFPISLKQSGPRDSLVQCFIKRNRNTQSYHLY 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LQEMRSRPHRVVHAAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSR-RNVVAC 65
                        PRIOR PILING DATE: 10/195, 906
PRIOR PILING DATE: 2002-07-15
PRIOR PILING DATE: 1999-11-01
PRIOR PILING DATE: 1999-11-01
PRIOR PELING DATE: 1999-11-01
PRIOR PELING DATE: 1999-11-01
PRIOR PELING DATE: 1998-11-11
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1998-04-02
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30, Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 LGLTTSLTDNGKFLLAASKLKR-----ATC----TDYI--
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CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2005-09-24
PRIOR FILING DATE: 2001-03-22
PRIOR FLING DATE: 2001-03-22
PRIOR PLING DATE: 2001-03-22
PRIOR PLING DATE: 2001-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-27
PRIOR PLING DATE: 2000-03-27
PRIOR PLING DATE: 2000-03-27
PRIOR PLING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PRELEED for Windows Version 3.0
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Pred. No. 3;
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Publication No. US2005025558A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Panka)
APPLICANT: Rizvi, Safia, K.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Kabnick, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-8
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Best Local Similarity 21.4%;
Matches 55; Conservative 3
      FILING DATE: 2003-07-31
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                                                                                                         APPLICANT: Helentjaris, Tim
APPLICANT: Cove, Keith
APPLICANT: Shen, Bo
APPLICANT: Shen, Bo
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
APPLICANT: Word PREDICANTON WUMBER: US/11/045,802
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: 60/541,122
PRIOR FILING DATE: 2004-02-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
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Sequence 8, Application US/11172145

Publication No. US20050272696A1

GENERAL INFORMATION:

APPLICANT: DeAngelis, Paul

TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC

TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS

TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS

CURRENT FILING DATE: 2005-06-30

CURRENT FILING DATE: 2004-06-30

PRIOR FILING DATE: 2003-06-15

PRIOR FILING DATE: 2003-08-15

PRIOR FILING DATE: 2003-08-16

PRIOR PRILING DATE: 2003-08-16

PRIOR PRILING DATE: 2003-08-16

PRIOR PRILING DATE: 2003-08-16

PRIOR PRILING DATE: 2003-08-16

PRIOR PRILING DATE: 2003-08-16

PRIOR FILING DATE: 2003-08-16

PRIOR FILING DATE: 2003-08-16

PRIOR PRILING DATE: 2003-08-16

PRIOR FILING DATE: 2003-06-18

PRIOR FILING DATE: 2003-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 -----YLGLTTSLTDN-- 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 -GKFLLAASKLKRATCTDYIIŞLR--SDDISKRSNAY-------LGRMRSN- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 --FLGTKFTVFDGSQTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 MRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPP 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 4.1%; Score 80.5; DB 7; Length 581; 1 Similarity 19.2%; Pred. No. 2.8; 61; Conservative 40; Mismatches 87; Indels 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 DLYLGT----FGTQEEAAE----
Sequence 30, Application US/11045802
Publication No. US20050257289A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 LVLSNKAPRWHEQLRCW 307
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                                                                                    APPLICANT: Gordon-Kamm, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Arabidopsis thaliana US-11-045-802-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 61; Conserv
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                                                                                                                                                                                                                                                       123 GLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKR------SNAYLGRM 169
                                                                                                                                                                                                                                                                                                                              170 RSNFLGTKFTVFDGSQTGAAKMQKSRSSNFIKV----SPRVPQGSYPIAHISYELNVL 223
                                                                                                                                                                                                                                                                                                                                                                                                       224 GS-----RGPRRMRCIMDTIP---MSIVESRGVVASTSISSFSSRSSPV--FRSHSKP 271
                                                                                                                                                                                           96
                                                                                                                                                         5 SLLQEMRSRPHRVVHAAASTANSSDPFSWSELPBELLREILIRVETVDGGDWP--SRRNV 62
                                                                                                                                                                                Gaps
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                                                                                  Query Match
4.1%; Score 80; DB 7; Length 483;
Best Local Similarity 21.9%; Pred. No. 2.4;
Matches 71; Conservative 51; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT '
US-11-137-465-41
'Sequence 41, Application US/11137465
'Sequence 41, Application US/11137465
'Publication No. US205025558A1
'GENERAL INFORMATION:
'APPLICANT: Adarwal, Paul R.
'APPLICANT: Mindcoh, Paul R.
'APPLICANT: Smith, Randall, F.
'APPLICANT: Kiang, Zahaoying
'APPLICANT: Kiang, Zahaoying
'APPLICANT: Kang, Zahaoying
'APPLICANT: Kang, Zahaoying
'APPLICANT: Kang, Zahaoying
'APPLICANT: Kang, Zahaoying
'APPLICANT: Kang, Zahaoying
'APPLICANT: Kang, Zahaoying
'APPLICANT: Kang, Zahaoying
'APPLICANT: Romick, Karen
'YEUR REBERENCE: GF50018
'CURRENT PILING DATE: 2002-09-24
'PRIOR FILING DATE: 2001-03-22
'PRIOR FILING DATE: 2001-03-24
'PRIOR FILING DATE: 2001-03-24
'PRIOR FILING DATE: 2000-03-24
'PRIOR FILING DATE: 2000-03-24
'PRIOR FILING DATE: 2000-03-27
'PRIOR FILING DATE: 2000-03-27
'PRIOR FILING DATE: 2000-03-27
'PRIOR FILING DATE: 2000-03-27
'PRIOR FILING DATE: 2000-04-27
'NUMBER: OF SEQ ID NOS: 66
'SEQ ID NO 41
'LENGTH: 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 FRELEALRSIDLAGNOLTRIPMGL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 LRSNSA--SCSDSGNNLGDPPLVL 293
              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-40
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Matches 71; Conserv
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LENGTH: 483
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5 SILOGEMRSRPHRVVHAAASTANSSDPFSWSELPEELLREILIRVETVDGGDWP--SRRNV |: : | | | | | : | | | | : | | : |

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                                                                                                                                                                                                                                                                                                                                                                                              224 GS------RGPRRMRCIMDTIP---MSIVESRGVVASTSISSFSSRSSPV--FRSHSKP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                  |: | || : : | | | : : | | | : : | 310 GNGLDRVPPALPRILAY--LPHNHYDALGARDLVATPGLTELMLAYNRLASARVHHRA 427
161 SVAPQFLPRSLRVADLAANQVMEIFPLTFGEKP--ALRSVYLHNNQLSNAGLPPDAFRGS 218
                                                       63 VACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLYL 122
                                                                                                                                                                    123 GLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKR------SNAYLGRM 169
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                                                                                                            219 EAIÁTLSLSNNOLSYLPPSLPPSLERLHLONNLISKVPRGAL-----SROTÓLRELYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Gaps
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4.1%; Score 80; DB 7; Length 1075;
Best Local Similarity 19.7%; Pred. No. 7.3;
Matches 62; Conservative 43; Mismatches 141; Indels
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CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/257,174
PRIOR FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2000-04-13
PRIOR PILING DATE: 2000-04-13
PRIOR PILING DATE: 2000-04-13
PRIOR PILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PEBESEQ for Windows Version 3.0
SERIOTH: 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
TILE OF INVENTION: NOVEL COMPOUNDS
FILLE OF THE GPSO22
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Publication No. US20050260714A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-174-150-34
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328 LKEIFSFPR--IHDALPISKEMSKLSNPKIP-----VYINICSI-----PSRIKQLQYT 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 AGV----CRSWRILTKEIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 ----ESIRDNGKFILLEKLIKENKDGYYITCDDDIRYPADYTNTMIKKINKYNDKAAIGL 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LQEMRSRPHRVVHAAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSR-RNVVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 615
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Sequence 2, Application US/11070627

Publication No. US20050271625A1

GENERAL IMPORMATION:

APPLICANT: Nash , Kevin R.

APPLICANT: Burger, Corinna

TILLE OF INVENTION: AAAV-NEPRILYSIN COMPOSITIONS AND METHODS OF US.

FILE REPERENCE: 36689.8

CURRENT APPLICATION NUMBER: US/11/070,627

CURRENT PILLING DATE: 2005-03-02

PRIOR APPLICATION NUMBER: 60/549,399

PRIOR FILING DATE: 2004-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.1%; Score 79.5; DB 7; Length 615;
Best Local Similarity 21.0%; Pred. No. 3.8;
Matches 54; Conservative 30; Mismatches 76; Indels 9
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                                                                                                  PILE REFERENCE: 35.24.104

PURRENT APPLICATION NUMBER: US/11/172,145

CURRENT FILING DATE: 2005-06-30

PRIOR PRILING DATE: 2005-06-30

PRIOR PLILING DATE: 2003-08-15

PRIOR PLILING DATE: 2003-08-15

PRIOR PLILING DATE: 2003-08-15

PRIOR PLILING DATE: 2003-08-15

PRIOR PLILING DATE: 2003-08-15

PRIOR PLILING DATE: 2003-08-16

PRIOR PLILING DATE: 2003-06-16

PRIOR PLILING DATE: 2003-07-31

PRIOR PRILING DATE: 2003-07-31

PRIOR PRILING DATE: 2003-07-31

PRIOR PLILING DATE: 10/195,908

PRIOR PLILING DATE: 1999-11-01

PRIOR PLILING DATE: 1999-11-01

PRIOR PLILING DATE: 1999-11-01

PRIOR PLILING DATE: 1999-11-11

PRIOR PLILING DATE: 1999-11-11

PRIOR PLILING DATE: 1999-11-11

PRIOR PLILING DATE: 1999-11-11

PRIOR PLILING DATE: 1999-04-01

PRIOR PLILING DATE: 1999-04-01

PRIOR PLILING DATE: 1999-04-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 ASKLKRATCTDYIISLR-----SDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAA 189
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                                                                                                                                                                                                                                                                                                                     SQUENCE 35, Application US/11174150
PUBLICATION NO. US20050260714A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: Singl, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP5002
CURRENT APPLICATION NUMBER: US/10/257,174
PRIOR PILING DATE: 2005-07-01
PRIOR PLING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
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                                                                                                                                                               : : |||:|
1048 GGASDTSASPPLLL 1061
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1087 GGASDTSASPPLLL 1100
                                                                                                                      280 SDSGNNLGDPPLVL 293
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ORGANISM: Homo sapiens
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APPLICANT: Brown, Eugene
APPLICANT: Lown, Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REPERRNET: AM 10.1079 (0.31896 - 0.10000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 TGAAKWOKSRSSNFIKVSPRVPQGSYPIAHISYELAVLGSRGPRRMRCIMDTIPMSIVES 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 RGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGD-----PPLVLSNKAPR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 QNRNNSCDSRGQTTKARFLYGE--NMPPQDAEIGYRNSLRQTNKTKQSCPFGRVPVNLLN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------RNTQSYHLYLGLTTSL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 TDNGKF---LLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 COLSTPYGOPACFOCOCH-QILATPLONLOVLASSSANECISVKGRIYSILKOIGSGGSS 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1635, Application US/10821234
Sequence 1635, Application US/10821234
Sublication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 W----HEQLRCWCLNFHGRVTVASVKNFQLVAVSDC-EAGQTSER---IILQFGKVG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%; Score 79; DB 6; Length 841;
19.6%; Pred. No. 6.5;
tive 62; Mismatches 175; Indels 132; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RSLLQEMRSR----PHRVVHAAASTANSSDPFSWSELPBELL--REILIRVETVDG--GDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 PSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISL-----KQSGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 SPDCDVKTDDSVVPCFMKRQTSRSECRDLVVPGSKPSGNDSCELRNLKS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 KVFQVLNEKKQIYAIKY---VNLEEADNQTLDSYRNEIA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 -----RDSLVQCFIKRN-------
                                                                                                             ; Sequence 88, Application US/10770726; Publication No. US20050266409A1; GENERAL INFORMATION:
402 PAMMISNNVSESANNVSGW 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 19.6
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-88
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                                                                      RESULT 13
US-10-770-726-88
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APPLICANT: Shen, Bo
APPLICANT: Shen, Bo
APPLICANT: Shen, Bo
APPLICANT: Tarczynaki, Mitchell
APPLICANT: Tarczynaki, Mitchell
APPLICANT: Tarczynaki, Mitchell
APPLICANT: Tarczynaki, Mitchell
APPLICANT: Tarczynaki, Mitchell
APPLICANT: Targer of Use
FILE REFERENCE: 035718/28674
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US/11/045,802
CURRENT FILING DATE: 2004-02-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NOS: 38
SEQ ID NOS: 38
SEQ ID NOS: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 RRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGD 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 TDNGKFLLAASKLKRATCTDYIISLR--SDDISKRSNAY--------LGRMRS 171
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-----AYDIAAIKF-----
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                                                                                                                                                                                                                                       35;
                                                                                                                                                                            5; DB 7; Length 750;
4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.0%; Score 79; DB 7; Length 584; Best Local Similarity 19.4%; Pred. No. 3.9; Matches 62; Conservative 39; Mismatches AA: ThAPle
                                                                                                                                                                                                                                    28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       356 K-PILTKYS-PRDL-----QNLMSWRFIMDLVSSLSRNYK 388
                                                                                                                                                                                                                                                                                                                                                                               90 TFPISLKOSGPRDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 KRNRNTQSY--HL-------YLG-----
                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                    4.1%; Score 79.5;
25.0%; Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-11-045-802-31
; Sequence 31, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
; APPLICANT: Gordon-Kamm, William
; ODT.ICANT: Helentjaris, Tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLVLSNKAPRWHEQLRCW 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.3
SEQ ID NO 2
LENGTH: 750
                                                                                            TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                    26; Conservative
                                                                                                                                                                                        Query Match
Best Local Similarity
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1027 SYKSÄVPFKILYNGOSVEVDĞHSMRKLİADLQPNTEYSFVLMNRGSSÄGGLQHLVSIRTA 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AC-AGVCRSWRILTKEIVAV-PEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------0NLHV- 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1087 PDLLPH-KPLPA-SAYIEDGRFDLSMPHVQDPSLVRWFYIVVVPIDRVGGSMLTPRW 1141
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                                                                                                                                                                                                                                                                                                                                                                                           14 PHRVVHAAASTANSSDPFSW---SELPEELL-----REILIRVETVDGGDWPSRRNVV
                                                                                                                                                                                                                                                                                                                 96;
                                                                                                                                                                                                                                                             DB 6; Length 1897;
20;
                                                                                                                                                                                                                                                                                                            38; Mismatches 138; Indels
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APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785C1P4CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      871 GLHKGTTYIFRLAAKNRAGLGEEFEKEIRTPEDLPSGFP----
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CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2001-02.55
PRIOR PELICATION NUMBER: 09/322,279
PRIOR PELICATION NUMBER: 09/32,279
PRIOR PELICATION NUMBER: 09/491,404
PRIOR PELING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/411,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/411,404
PRIOR PELING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/611,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
                                                                                                                                                                                                                                                             4.0%; Score 79;
23.8%; Pred. No. 2
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1635
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Wang, Zhiwei
Wehrman, Tom
                                                                                                                                                                                                                                                                                                            85; Conservative
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                              US-10-821-234-1635
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                                                                                                                                         LENGTH: 1897
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1037 SYKSAVPFKILYNGOSVEVDGHSMRKLIADLOPNTEYSFVLMNRGSSAGGLOHLVSIRTA 1096
                                                                                                                                                                                                                                                                                                                 150 IISLRSDDISKRSNAYLGRMRSNFLGTKFTVFDGSQTGAAKMQKSRSSNFIKVSPRVPQG 209
                                                                                                                                                                                                                                                                                                                                                                             64 AC-AGVCRSWRILTKEIVAV-PEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLY 121
                                                                                                                                                                                                                                                                                                                                                                                                                       -----QNLHV- 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         925 TGLTTSTTELAWDPPVLAERNGRIISYTVVFRDINSQOELONITTDTRFTLTGLKPDTTY 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 SYPIA---HISYELNVLGSRGPRRMRCIMDTIPMS----IVESRGVVASTSISSFSSRSS 262
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                                                                                                                                                                                                                                                                                      ----REILIRVETVDGGDWPSRRNVV
                                                                                                                                                                                                                                          96; Gaps
                                                                                                                                                                                            Query Match
4.0%; Score 79; DB 7; Length 1907;
Best Local Similarity 23.8%; Pred. No. 20;
Matches 85; Conservative 38; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         14 PHRVVHAAASTANSSDPFSW---SELPEELL--
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 250
LENGTH: 1907
                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-11-000-463-250
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Search completed: December 23, 2005, 23:29:44 Job time : 17 secs

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December 23, 2005, 22:46:55; Search time 198 Seconds (without alignments) 843.252 Million cell updates/sec
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version 5.1.6
- 2005 Compugen Ltd.
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ALIGNMENTS

Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 944. plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism. ADN73049 standard; protein; 380 AA. (first entry) 15-JUL-2004 ADN73049; RESULT 1 ADN73049

20-OCT-2003; 2003WO-EP011658. Arabidopsis thaliana. WO2004035798-A2. 29-APR-2004.

Vlieghe K; 18-OCT-2002; 2002EP-00079408. De Veylder L, (CROP-) CROPDESIGN NV Inze D,

WPI; 2004-348466/32. N-PSDB; ADN73048.

Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or more proteins.

Claim 1; SEQ ID NO 944; 134pp; English.

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are upon down-regulated in transgenic plants overexpressing the heterodimeric ESFA/DPA transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture

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or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/ or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing the EZFa/DPa transcription factor, given in an exemplification of the
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The invention relates to Arabidopsis TUBBY-like proteins (TLP) and their corresponding nucleic acid sequences. The invention also relates to a transformed cell or a transgenic plant containing TLP nucleic acid and a transformed cell or a transgenic plant lacking TLP nucleic acid and a polypeptides and nucleic acids are useful for producing transgenic or transformed cells or plants having higher tolerance to salt, chilling, pathogens, oxidative stress or water-deficit. The present sequence is the Arabidopsis thaliana TLP 9 protein.

Sequence 380 AA;

New isolated Arabidopsis TUBBY-like proteins, useful for producing transgenic or transformed cells or plants having higher tolerance tsalt, chilling, pathogens, oxidative stress, or water-deficit.

2005-080955/09.

N-PSDB; ADW64874.

Claim 1; SEQ ID NO 9; 43pp; English.

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Arabidopsis thaliana TUBBY-like protein (TLP) 9.

Arabidopsis thaliana

US2005014266-A1.

20-JAN-2005

(first entry)

07-APR-2005

ADW64863;

21-JAN-2004; 2004US-00763042 21-JAN-2003; 2003US-0441380P

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ADW64863 standard; protein; 380

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                 TQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                     181 GTKFTVFDGNLLPSTGAAKDRKSRSYNPAKVSAKVPLGSYPVAHITYELNVLGSRGPRKM
                                                                                   GTKFTVFDGS----QTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRM
                                                                                                                                                   RCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPL
                                                                                                                                                                                                                     VLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAV-SDCEAG-----QTSERIILQF
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                                                                                                                                                                                                                                                                       New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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MTLRSLILEMRSRPHRVVHDLAAAAADSTSVSSQDYRWSEIPBELLREILIRVEAADGG
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Sherman BK;
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                                                                                                                                                                   cliffe O, Creelman RA,
Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 462; 510pp; English
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                                                                                                                                                                   Ratcliffe O,
                                                                                                                                 (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                 17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                              18-SEP-2003; 2003WO-US030292
                                                                 18-SEP-2002; 2002US-0411837P
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N-PSDB; ADO61994.
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                                                                                                                                                                                                                                      TQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFL
                                                                                                                                                                   GTKFTVPDGS----QTGAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRM
                                                                                                                                                                                                                QCLMDTIPTSTMEPQGVASEPSEPPLLGTRSTLSRSQSKPLRSSS-----SHLKETPL
                                                                         MTPRSLLQEMRSRPHRVVH-----AAASTANSSDPPSWSELPBELLREILIRVETVDGG
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Arabidopsis TUBBY-like proteins, useful for producing transgenic or transformed cells or plants having higher tolerance to salt, chilling, pathogens, oxidative stress, or water-deficit.
                                                                                                                                                                                                                                                                                                                                                                           Transgenic plant; salt tolerance; crop improvement; cold tolerance; oxidative stress; drought resistance; TUBBY-like protein; plant.
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8 54; Indels
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32; Mismatches
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99US-0161361P.
99US-0161920P.
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99US-0161993P.
99US-0162142P.
                                             73.3%;
72.5%;
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                                                  Local Similarity ...
les 287; Conservative
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26-0CT-1999;
28-0CT-1999;
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The invention relates to Arabidopsis TUBBY-like proteins (TLP) and their corresponding nucleic acid sequences. The invention also relates to a transformed cell or a transgenic plant containing TLP nucleic acid and a transformed cell or a transgenic plant lacking TLP nucleic acid. The polypeptides and nucleic acids are useful for producing transgenic or transformed cells or plants having higher tolerance to salt, chilling, pathogens, oxidative stress or water-deficit. The present sequence is the Arabidopsis thaliana TLP 11 protein.
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                                                                                                                                                                                                                                                                                                                  72.1%; Score 1414.5; DB 9; 72.9%; Pred. No. 2.1e-149; ive 31; Mismatches 51;
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US-0126785P UUS-0121462P UUS-0128134P UUS-012814P UUS-0130077P UUS-0130077P UUS-0130891P UUS-0131449P UUS-0131449P UUS-0132464P UUS-0132484P	99US-013487P. 99US-013484P. 99US-0134218P. 99US-0134218P. 99US-0134219P. 99US-013421P. 99US-013431P. 99US-013434P. 99US-0135353P. 99US-0135353P. 99US-0135353P. 99US-013552P. 99US-013552P. 99US-013552P. 99US-013552P. 99US-013552P. 99US-013552P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013752P. 99US-013452P. 99US-013452P. 99US-013455P. 99US-013455P. 99US-013455P.	905 - 01394600 905 - 01394612 905 - 01394612 905 - 01394612 905 - 01397631 905 - 01403513 905 - 01403513 905 - 01406912 905 - 01406912 905 - 01412871 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513 905 - 01420513
- MAR. 1999 1- APR-1999 3- APR-1999 3- APR-1999 9- APR-1999 9- APR-1999 9- APR-1999 9- APR-1999 9- APR-1999 9- APR-1999 9- APR-1999	0.6-WAY-1999; 10.7-WAY-1999; 14-WAY-1999; 14-WAY-1999; 14-WAY-1999; 14-WAY-1999; 19-WAY-1999; 20-WAY-1999; 21-WAY-1999; 22-WAY-1999; 22-WAY-1999; 01-JUN-1999; 01-JUN-1999; 01-JUN-1999; 01-JUN-1999; 01-JUN-1999; 11-JUN-1999;	8-UN-1999 8-UN-1999 8-UN-1999 8-UN-1999 1-UN-1999
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PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144333P.
PR 20-JUL-1999; 99US-0144333P.
PR 20-JUL-1999; 99US-0144333P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144841P.
PR 20-JUL-1999; 99US-0144841P.
PR 21-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014531P.
PR 22-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014531P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-0143331P.
PR 23-JUL-1999; 99US-0143331P.
PR 23-JUL-1999; 99US-014331P.
PR 23-JUL-1999; 99US-0143331P.
PR 23-SEP-1999; 99US-0143331P.
PR 23-SEP-1999; 99US-0143331P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1999; 99US-0153303P.
PR 23-SEP-1

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This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Bucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait of the plant such as increased drought, salt or disease tolerance, height change, enhanced cold/ frost tolerance, enhanced color, health and nutritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

Composition, flower longevity and germination, amongst others.

Composition, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polypeptide is a plant transcription factor protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EVLVKIEASE-GSWPSRKSVVACAGVCRSWRHLVKEIVKVPEVSGILTFPISVKQPGPRE 119
plant, transcription, gene regulation, gene expression, transgenic plant, drought resistance, disease resistance, salt tolerance, cold tolerance, freezing tolerance, flowering, flavor enhancer, flower color.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 ELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSS----RSSPVFRSHSKPLRS 274
                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 ELNVLGSRGPRRMHCTMDAIPASAIEAGGVAPTQTELPLSSVEFPSLPFFRT-----KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIFRSILQEMRSRPHRVVH-------AAASTANSSDPFS---WSELPEBLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BILIRVETVDGGDWPSRRNVVACAGVCRSWRILLTKBIVAVPEFSSKLTFPISLKQSGPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SLLQCFIKRNRSNQTYHLYVGLTNALSDDGKFLLAARKCRRPTCTDYVISLHADDVSKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 NAYLGRARSNFLGTKFTVFDGSQT-GAAKMQKSRSSNF1---KVSPRVPQGSYPIAHISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Gaps
                                                                                                                                                                                                                                                         Frost MJ;
1 ST, Magusin A;
Gause K, Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.0%; Score 1215.5; DB 9; Length 403; 60.6%; Pred. No. 5.7e-127; ive 49; Mismatches 77; Indels 35;
                                                                                                                                                                                                                                                         Connett MB, Emerson SJ, F
Higgins C, Lasham A, Lund
Veerakone S, Westwood C,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 31; SEQ ID NO 1241; 1265pp; English.
                                                                                                                                                           07-JUN-2004; 2004WO-US017965
                                                                                                                                                                                           06-JUN-2003; 2003US-0476189P
                                                                                                                                                                                                                                                         Bloksberg LN, Bryant C,
Forster RLS, Grigor M,
Phillips J, Puthigae S,
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                                                                                                                                                                                                                           (ARBO-) ARBORGEN LLC.
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                                                               Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADW16693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 403 AA;
                                                                                             WO2005001050-A2
                                                                                                                             06-JAN-2005
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Best Local Si
Matches 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ACAGVCRGWRLLMNETVVVPEISSKLTFPISLKQPGPRDSLFQCFIKRNRTTQSYHLYLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIVESRGVVASTSISSFSSRSSPVFRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEQLRCWCLNFHGRVTVASVKNFQLVAV-SDCEAG-----OTSERIILQFGKVGKDMFT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 HEQLRCWCLNFHGRVTVASVKNFQLVAAGASCGSGTGMSPERQSERIILQFGKVGKDMFT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S---OTGAAKMOKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDTIPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eucalyptus grandis transcription factor protein TUBBY family Seg 1241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRSRPHRVVH-----AAASTANSSDPFSWSELPEELLREILIRVETVDGGDWPSRRNVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.8%; Score 1409.5; DB 3
72.6%; Pred. No. 7.8e-149;
.ive 31; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z
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                            9903-0159294P.
9903-0159295P.
9903-0159329P.
9903-0159330P.
                                                                                                                                                         99US-0160741P.
99US-0160767P.
99US-0160768P.
99US-0160770P.
                                                                                                           99US-0159637P.
99US-0159638P.
99US-0159584P.
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99US-0160980P.
99US-0160981P.
99US-0160989P.
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99US-0161405P.
99US-0161406P.
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99US-0161993P.
99US-0161993P.
99US-0162142P.
99US-0158369P
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99US-0161361P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
             13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
12-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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26-OCT-1999;
26-OCT-1999;
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ADW17479
ID ADW1
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AC ADW1
XX
DT 24-M
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This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and pinus radiata. The present transcription factor that regulates the promoter, which is operably transgenic plants expressing a transcription factor that regulates the promoter, which is operably ransgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height change, enhanced cold/ frost tolerance, enhanced color, health and nutritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

Composition, flower longevity and germination, amongst others.

Composition are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polypeptide is a plant transcription factor protein sequence of the invention.
                  plant, transcription, gene regulation, gene expression, transgenic plant, drought resistance, disease resistance, salt tolerance, cold tolerance; freezing tolerance, flowering, flavor enhancer, flower color.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connett MB, Emerson SJ, Frost MJ;
Higgins C, Lasham A, Lund ST, Magusin A;
Veerakone S, Westwood C, Gause K, Wood M;
                                                                                                                                                                                                                                                                                                                                 Eucalyptus grandis transcription factor protein TUBBY family Seq 1242.
NSASCSDSGNNLG--DPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSDCE
                                                                      Claim 31; SEQ ID NO 1242; 1265pp; English.
                                                                                                                                                                                                                ADW17480 standard; protein; 408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2004; 2004WO-US017965
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Forster RLS, Grigor M,
Phillips J, Puthigae S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bloksberg LN, Bryant C,
Forster RLS, Grigor M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ARBO-) ARBORGEN LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-075542/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADW16694.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2005001050-A2.
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                                    295
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up - or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where
                                             100
                                                                                                                             LRDVIAMRIEKSE-STWPPRKNVVACAGVCRNWREIMKEIVKTPEVSGKLTFPISLKQPGP 121
                                                                                                           RDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISK 160
                                                                                                                                                                                                                                        SYELINVIGSRGPRRMRCIMDTIPMSIVESRGVV-----ASTSISSFSSRSSPVFRSHSK 270
                                                                                                                                                                                                                                                                                                      271 PLRSNSASCSDSGNNLGDPP---LVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVA 327
                                                                                                                                                                                                                                                                                                                          Thale cress protein upregulated in E2Fa/Dpa expressing plants SegID 1300.
             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Altering plant characteristics, useful for producing plants for enzyme cypharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
:|:|| || || : :| :: |: |: || || || SEKSIIQDVKDEIGNISRKGFDHVKFGYGLRSRSHRVVQDSSVVVDALKQSCWASMPPEL
                                                                                                                                                                                           242 SYELNVIGSRGPRRMQCVLDAIPASSIEPGGVAPTQTEFVSSTLDTFPSFS--FFRS--
                                             LREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGP
                                                                                                                                                                         161 RSNAYLGRMRSNFLGTKFTVFDGSQTGA-AKMQKSRSS---NFIKVSPRVPQGSYPIAHI
                                                                                                                                                                                                                                                                                                                                                                      328 VSD-CEAGQISERIILQFGKVGKDMFTWDYGYPISAFQAFAICLSSFETRIACE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1300; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN73405 standard; protein; 406 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
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43;

79; Indels

58.8%; Score 1153.5; DB 9; 56.0%; Pred. No. 5.5e-120; iive 60; Mismatches 79;

Conservative

232;

Best Loca Matches

Query Match Best Local Similarity

TFRSLLQE-----

Length 408;

----MRSRPHRVVHAAASTANSSDPFSWSELPEEL 40

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biomass, enhanced surrival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilibation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/ or carbon metabolism or they function as
                                                                                                                                                                                                                                                                                                                 transcription factors. This polypeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing the B2Fa/DPa transcription factor, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 GSNTYIĞKLRSNFLGTKFTVYDAQPTNPGTQVTRTRSSRLLSLKQVSPRIPSGNYPVAHI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 DSLVQCFIKRNRNTQSYHLYLGLTTSLT-DNGKFLLAASKLKRATCTDYIISLRSDDISK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYELNVIGSRGPRRMRCIMDTIPMSIVESRGV-----VASTSISSFSSRSSPVFRSHSK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 SYELNVLGSRGPRRMQCVMDAIPASAVEPGGTAPTQTELVHSNLDSPPSFS--FFR--SK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 PLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAV-S 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 SIRAESLIPSGPSSAAQKEGLLVLKNKAPRWHEQLQCWCLNFNGRVTVASVKNFQLVAAPR 355
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characteristics are selected from increased yield or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSFKSLIQDMRGELGSISRKGFDVRFGYGRSRSQRVVQDTSVPVDAFKQSCWASMPPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSNAYLGRMRSNFLGTKFTVFDGSQTG-AAKMQKSRSSNFI---KVSPRVPQGSYPIAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RSRPHRVVHAAASTANSSDPFSWSELPEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic plant; salt tolerance; crop improvement; cold tolerance; oxidative stress; drought resistance; TUBBY-like protein; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.6%; Score 1149; DB 8; 56.7%; Pred. No. 1.8e-119; ive 58; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana TUBBY-like protein (TLP) 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2004; 2004US-00763042
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Best Local Similarity 56.7
Matches 233; Conservative
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       altered plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 PLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAV-S 329
                                                                                                                                                                            The invention relates to Arabidopsis TUBBY-like proteins (TLP) and their corresponding nucleic acid sequences. The invention also relates to a transformed cell or a transgenic plant containing TLP nucleic acid and a transformed cell or a transgenic plant lacking TLP nucleic acid. The TLP polypeptides and nucleic acids are useful for producing transgenic or transformed cells or plants having higher tolerance to salt, chilling, pathogens, oxidative stress or water-deficit. The present sequence is the Arabidopsis thaliana TLP 3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 DSLVQCFIKRNRNTQSYHLYLGLTTSLT-DNGKFLLAASKLKRATCTDYIISLRSDDISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 SYELNVLGSRGPRRRQCVMDAIPASAVEPGGTAPTQTELVHSNLDSFPSFS--FFR--SK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 RSNAYLGRMRSNFLGTKFTVFDGSQTG-AAKMQKSRSSNF1---KVSPRVPQGSYPIAHI
                                                                                                                                                                                                                                                                                                                                                                                                                    ---RSRPHRVVHAAASTANSSDPFSWSELPEELL
                                                                                                                                                                                                                                                                                                                                                                                      36; Gaps
                                                                                     New isolated Arabidopsis TUBBY-like proteins, useful for producing transgenic or transformed cells or plants having higher tolerance salt, chilling, pathogens, oxidative stress, or water-deficit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 DCEAGQISERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE 380
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                                                                                                                                                                                                                                                                                                                                                       Score 1149; DB 9;
Pred. No. 1.8e-119;
58; Mismatches 84;
                                                                                                                                                    Claim 1; SEQ ID NO 3; 43pp; English.
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Best Local Similarity 56.7
Matches 233; Conservative
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                                                           N-PSDB; ADW64868
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                                               25-FEB-2000;
                  06-SEP-2000
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plant; transcription; gene regulation; gene expression; transgenic plant; drought resistance; disease resistance; salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer; flower color.

07-JUN-2004; 2004WO-US017965 06-JUN-2003; 2003US-0476189P

WO2005001050-A2 Pinus radiata

06-JAN-2005

Pinus radiata transcription factor protein TUBBY family Seq 1627

24-MAR-2005 (first entry)

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78 EIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLA 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 RSYNPAKVSAKVPLGSYPVAHITYELAVLGSRGPRKMQCLMDTIPTSTMEPQGVASEPSE 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.2%; Score 1142.5; 73.2%; Pred. No. 6e-11:ive 26; Mismatches
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99US-0160741P.
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22-SEP-1999, 23-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SEP-1999, 28-SE
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This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Bucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a cranscription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait of the plant such as increased drought, salt or disease tolerance, height change, enhanced cold/ frost tolerance, enhanced color, health and nutritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

Composition, flower longevity and germination, amongst others.

Composition, flower longevity and difference in flower color, petal or leaf shape and size, aroma or plant height. This polypeptide is a plant transcription factor protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTFRSLLQE------WRSRPHRVVHAAASTANSSDPFS-WSELPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 LLREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSG
                                                                                                                                                                                                                                                                                                                                                                                    Connett MB, Emerson SJ, Frost MJ;
Higgins C, Lasham A, Lund ST, Magusin A;
Veerakone S, Westwood C, Gause K, Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 31; SEQ ID NO 1627; 1265pp; English.
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Forster RLS, Grigor M,
Phillips J, Puthigae S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 54.4
hes 224; Conservative
                                                                                                                                                                                                                                                                                                                                                 (ARBO-) ARBORGEN LLC.
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ADW17849 standard; protein; 411 AA.

RESULT 12 ADW17849 ID ADW1 XX ä

Gaps

52;

88; Indels

55.1%; Score 1082; DB 9; 53.2%; Pred. No. 6.3e-112; ive 59; Mismatches 88;

Query Match Best Local Similarity 53.2³ Matches 226; Conservative

Length 418;

153

93 9

SLKOSGPRDSLVQCFIKRNRNTQSYHLYLGLTTSLTDNGKFLLAASKLKRATCTDYIISL

94

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1 MTFRSLLQEM------RSRPHRVV-----HAAASTANSSDPFS----W

1 MTVKNIFODMKGSIGSISRRSFEVKFLRSRSQSAVDDLHYRSNANNKNNSNNGGLQCSLW 34 SELPEELLREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPI

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154 RSDDISKRSNAYLGRMRSNFLGTKFTVFDG----SQTGAAKMOKSRSSNFIKVSPRVPQG

240 SYNIAHIGYELNVLGTRGPRRMQCIMHSIPASAVQPGGSAPTPVEPSVASLDQSLASCPT

SYPIAHISYELNVLGSRGPRRMRCIMDTIPMSIVESRG-----VVASTSISSFSSRSSPV

210

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300 FGSKSCILESSSISEPLITGSNLKDEPLVIKNKAPRWHEQLQCWCLNFKGRVTVASVKNFQ

PRSHSKPLRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQ

265

376 RIACE 380

ADW17850 standard; protein; 418 AA.

RESULT 14 ADW17850 24-MAR-2005 (first entry)

ADW17850;

LVAV------SDCEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFET

325

264

413

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plant; transcription; gene regulation; gene expression; transgenic plant; drought resistance; disease resistance; salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer; flower color.
                                                                                          240 IAYELMVLGTRGPRRMQCI.MDAVPASAMEAGGSAPTPTECPLSSLDSLATLPHLGLKSEV 299
                                                                                                                                                                                                                     300 IETSFFSGPIINSNWKEGPLILLKNKAPRWHEQLQCWCLNFKGRVTVPSVKNFQLVAATEP 359
RGSNRYIGKLRSNFLGTKFTIYDSQPPCTGAIASTSRGSRRVGSKQVSPRVPAGSYVVAH 239
                                                          ISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSH----SKP 271
                                                                                                                                                                                        LRSNSASCSDSGNNLGDPPLVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSD- 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynuclectides isolated from plants encoding transcription factors, and polypeptides encoded by such polynuclectides, useful for regulating gene transcription and gene expression.
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Lund ST, Magusin A;
I C, Gause K, Wood
                                                                                                                                                                                                                                                                                                                --CEAGQTSERIILQFGKVGKDMFTMDYGYPISAFQAFAICLSSFETRIACE 380
                                                                                                                                                                                                                                                                                                                                                 Pinus radiata transcription factor protein TUBBY family Seq 1629.
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Higgins C, Lasham A, Lund
Veerakone S, Westwood C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADW17851 standard; protein; 418
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Forster RLS, Grigor M,
Phillips J, Puthigae S,
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plant; transcription; gene regulation; gene expression; transgenic plant; drought resistance; disease resistance; salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer; flower color.
                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating
                                                                                                                                                                                                                                                                                                                        Lund ST, Magusin A;
| C, Gause K, Wood M;
                                                                        Pinus radiata transcription factor protein TUBBY family Seq 1628.
                                                                                                                                                                                                                                                                                                             Frost MJ
                                                                                                                                                                                                                                                                                                           Connett MB, Emerson SJ,
Higgins C, Lasham A, Lund
Veerakone S, Westwood C,
                                                                                                                                                                                                                                07-JUN-2004; 2004WO-US017965.
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                                                                                                                                                                                                                                                                                                             , Bryant C,
Grigor M, P
Puthigae S,
                                                                                                                                                                                                                                                                                     (ARBO-) ARBORGEN LLC.
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N-PSDB; ADW17064.
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Forster RLS, G
Phillips J, Pu
                                                                                                                                                     Pinus radiata
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This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Bucalyptus grandis and Plans radiata. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height change, enhanced cold frost tolerance, enhanced color, health and nutritional characteristics, as well as improved taste, starch cutritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others. Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polypeptide is a plant transcription factor protein sequence of the invention.

Sequence 418 AA;

Claim 31; SEQ ID NO 1629; 1265pp; English.

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                                                     variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiate. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height composition, flower longevity and germination, amongst others.

Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polypeptide is a plant transcription factor protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant; transcription; gene regulation; gene expression; transgenic plant; drought resistance; disease resistance; salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer; flower color.
                                             invention relates to novel isolated plant nucleic acid molecules, or
                                                                                                                                                                                                                                                                                                                                                                                           NVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLKQSGPRDSLVQCFIKRNRNTQSYHL 120
                                                                                                                                                                                                                                                                                                                                                                                                         89 NVVVCAGVCRTWREIIKEIVKPPLLSGVLTPPVSLKQPGPKDSAVQCFIKQDRTASAYYL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                           YLGLTTSLTDNGKFLLAASKLKRATCTDYIISLRSDDISKRSNAYLGRMRSNFLGTKFTV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDGSQT---GAAKMQKSRSSNFIKVSPRVPQGSYPIAHISYELNVLGSRGPRRMRCIMDT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 IPMSIVE-----SRGVVASTSISSFSS-RSSPVFRSHSKPLRSNSASCSDSGNNLGDPP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 IPASVVEGGLNTSTFEIPSSTLVBPLASFRSS---RSKSVISESNAFSGPLNSGNLKDDP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVLSNKAPRWHEQLRCWCLNFHGRVTVASVKNFQLVAVSDCEAGQTSE----RIILQFGK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                        RSRPHRVVHAAASTANSSD-----PFSWSELPEELLREILIRVETVDGGDWPSRR
                                                                                                                                                                                                                                                                                                                   31; Gaps
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                                                                                                                                                                                                                                                                                            DB 9; Length 418;
                                                                                                                                                                                                                                                                                          53.5%; Score 1049.5; DB 9; Length 54.8%; Pred. No. 2.9e-108; Live 57; Mismatches 90; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 VGKDFFTWDYRYPLSAFQAFAICLSSFDTKLACE 418
                     Claim 31; SEQ ID NO 1628; 1265pp; English.
transcription and gene expression.
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                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.8#
Matches 216; Conservative
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                                                                                                                                                                                                                                                                    Sequence 418 AA;
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  gene
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This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a cranscription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait of the plant such as increased drought, salt or disease tolerance, height change, enhanced cold/ frost tolerance, enhanced color, health and contritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

Composition, flower longevity and germination, amongst others.

Composition, flower longevity and difference in flower color, petal or leaf shape and size, aroma or plant height. This polypeptide is a plant transcription factor protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynuclectides isolated from plants encoding transcription factors, and polypeptides encoded by such polynuclectides, useful for regulating gene transcription and gene expression.
                                                                                                                                                                                                                                                                                                                    Magusin A;
e K, Wood M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 PEELLREILIRVETVDGGDWPSRRNVVACAGVCRSWRILTKEIVAVPEFSSKLTFPISLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 NIANIVYELNVLGTRGPRRMQCTWHSIPASSIQVGGNAPTPTEFPRSLDESFSLPFSKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSLRSIMREIKEVRNGIGNISRRRSFDMRVSHNHRARSQATIDDTLSRVLFVQQSQWANL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 PIAHISYELNVLGSRGPRRMRCIMDTIPMSIVESRGVVASTSISSFSSRSSPVFRSHSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDISKRSNAYLGRMRSNFLGTKFTVFDGS--QTGAAKMOKSRSSNFI--KVSPRVPQGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SJ, Frost MJ;
Lund ST, Magui
d C, Gause K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                           Emerson SJ,
                                                                                                                                                                                                                                                                                        Connett MB, Emerson SJ,
Higgins C, Lasham A, Lund
Veerakone S, Westwood C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.4%; Score 1028; DB 9; I Best Local Similarity 53.0%; Pred. No. 7.4e-106; Matches 220; Conservative 57; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 31; SEQ ID NO 2296; 1265pp; English.
                                                                                                                07-JUN-2004; 2004WO-US017965.
                                                                                                                                                                        06-JUN-2003; 2003US-0476189P.
                                                                                                                                                                                                                                                                                        Bloksberg LN, Bryant C,
Forster RLS, Grigor M,
Phillips J, Puthigae S,
                                                                                                                                                                                                                             (ARBO-) ARBORGEN LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-075542/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADW18185
WO2005001050-A2
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                                                           06-JAN-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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